

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2003, 08:08:56 ; Search time 29.7313 Seconds
(without alignments)
268.471 Million cell updates/sec

Title: US-09-928-048A-4
Perfect score: 422
Sequence: 1 VSEIQLMHNLGRHLSMERY.....KSLGRANKADVNVLYKAKSQ 83

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	417	98.8	115	1	PTHU
2	366	86.7	115	2	JC4202
3	359	85.1	115	1	PTHU
4	355	84.1	115	1	PTHU
5	311	73.7	115	2	A05091
6	303	71.8	105	2	I51851
7	174.5	41.4	119	2	A34937
8	73	17.3	565	2	G89813
9	72.5	17.2	824	2	F72408
10	72	17.1	1257	1	I58383
11	69.5	16.5	555	2	T44010
12	67.5	16.0	1156	2	B70356
13	67	15.9	443	2	E82046
14	67	15.9	655	2	C71438
15	67	15.9	378	2	B71438
16	66.5	15.8	674	2	F56653
17	66	15.6	215	2	T33195
18	66	15.6	396	2	G96934
19	66	15.6	1163	2	F84669
20	65	15.4	1284	2	H86803
21	65	15.4	1244	2	T23744
22	64.5	15.3	205	2	A86506
23	64.5	15.3	205	2	F72117
24	64.5	15.3	1018	2	T40253
25	64	15.2	166	2	T43497
26	64	15.2	642	2	D81401
27	63.5	15.0	417	2	E70207
28	63.5	15.0	487	2	A71407
29	63.5	15.0	797	2	A96232

30	63.5	15.0	797	2	AD3054
31	63.5	15.0	1270	2	T09194
32	63	14.9	108	2	T37558
33	63	14.9	672	2	T42186
34	63	14.9	862	2	A05028
35	63	14.9	992	2	A39331
36	63	14.9	1000	2	S18827
37	63	14.9	1033	2	S73693
38	63	14.9	1937	2	I38055
39	63	14.9	2109	2	I38414
40	63	14.9	5005	2	F82884
41	62.5	14.8	370	1	D64550
42	62.5	14.8	415	2	T34156
43	62.5	14.8	509	2	T29291
44	62.5	14.8	673	2	S54182
45	62.5	14.8	674	2	S54178

ALIGNMENTS

RESULT 1

PTHU
parathyroid hormone precursor (validated) - human
N:Alternate names: parathyroid hormone
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1984 #sequence_revision 19-Jan-1996 #text_change 08-Dec-2000
C:Accession: A19339; S53790; A93169; S21199; A93789; A93783; A90387; A90426; A94
R:Vasicek, T.J.; McDevitt, B.E.; Freeman, M.W.; Fennick, B.J.; Hendy, G.N.; Pott
proc. Natl. Acad. Sci. U.S.A. 80, 2127-2131, 1983
A:Title: Nucleotide sequence of the human parathyroid hormone gene.
A:Reference number: A19339; MUID:83169834; PMID:6220408
A:Accession: A19339
A:Molecule type: DNA
A:Residues: 1-115 <VAS>
A:Cross-references: GB:J00301; NID:9190702; PIDN:AAA0215.1; PID:9190704
R:Yamaguchi, T.; Fukase, M.; Sugimoto, T.; Kido, H.; Chihara, K.
Biol. Chem. Hoppe-Seyler 375, 821-824, 1994
A:Title: Purification of meprin from human kidney and its role in parathyroid ho:
A:Reference number: S53790; MUID:95225988; PMID:7710697
A:Accession: S53790
A:Molecule type: protein
A:Residues: X',33,X',35-46:65-84;105-110 <YAM>
A:Note: peptides generated in vitro and in vivo by meprin; peptide cleavage also
R:Jacobs, J.W.; Kemper, B.; Miall, H.D.; Habener, J.F.; Potts Jr., J.T.
Nature 249, 155-157, 1974
A:Title: Structural analysis of human parathyroid hormone by a new microsequen
A:Reference number: A93169; MUID:74174967; PMID:4833316
A:Accession: A93169
A:Molecule type: protein
A:Residues: 26-37 <JAC>
R:Olstad, O.K.; Reppe, S.; Gabrielsen, O.S.; Hartmanis, M.; Blingsmo, O.R.; Gaut
Eur. J. Biochem. 205, 311-319, 1992
A:Title: Isolation and characterization of two biologically active O-glycosylate
A:Reference number: S21199; MUID:92209518; PMID:1555591
A:Accession: S21199
A:Molecule type: protein
A:Residues: 32-114,N' <OLS>
A:Note: cloned sequence expressed in Saccharomyces cerevisiae exhibited O-glycosyl
R:Niall, H.D.; Sauer, R.T.; Jacobs, J.W.; Keutmann, H.T.; Segre, G.V.; O'Riordan,
Proc. Natl. Acad. Sci. U.S.A. 71, 384-388, 1974
A:Title: The amino-acid sequence of the amino-terminal 37 residues of human parat
A:Reference number: A93789; MUID:74111656; PMID:4521809
A:Accession: A93789
A:Molecule type: protein
A:Residues: 32-68 <NIA>
R:Brewer Jr., H.B.; Fairwell, T.; Ronah, R.; Sizemore, G.W.; Arnaud, C.D.
Proc. Natl. Acad. Sci. U.S.A. 69, 3585-3588, 1972
A:Title: Human parathyroid hormone: amino-acid sequence of the amino-terminal res
A:Reference number: A93783; MUID:73070429; PMID:4509319
A:Accession: A93783
A:Molecule type: protein

hypothetical prote
adaptor protein in
probable methyltra
conserved hypotet
rpoC protein homol
protein-tyrosine k
Flt3 protein - mou
MG328 homolog p01
myosin heavy chain
transcription fact
hypothetical prote
probable membrane
hypothetical prote
hypothetical prote
low affinity penic
low affinity penic

A:Residues: 32-52,'Q',54-58,'K',60,'L',62-65 <BRE>
 A:Note: this sequence was determined by sequenator and mass spectroscopic identification
 R:Keutmann, H.T.; Niall, H.D.; O'Riordan, J.L.H.; Potts Jr., J.T.
 Biochemistry 14, 1842-1847, 1975
 A:Title: A reinvestigation of the amino-terminal sequence of human parathyroid hormone.
 A:Reference number: A90387; MUID:75146516; PMID:1125201
 A:Accession: A90387
 A:Molecule type: protein
 A:Residues: 52-75 <KE3>
 R:Keutmann, H.T.; Sauer, M.M.; Hendy, G.N.; O'Riordan, J.L.H.; Potts Jr., J.T.
 Biochemistry 17, 5723-5729, 1978
 A:Title: Complete amino acid sequence of human parathyroid hormone.
 A:Reference number: A90426; MUID:79082855; PMID:728431
 A:Accession: A90426
 A:Molecule type: protein
 A:Residues: 61-106,'D',108-115 <KEU>
 R:Keutmann, H.T.; Niall, H.D.; Jacobs, J.W.; Barling, P.M.; Hendy, G.N.; O'Riordan, J.L.H.
 in Calcium-regulating Hormones, Talmadge, R.V., Owen, M., and Parsons, J.A., eds., pp.9-11
 A:Reference number: A94410
 A:Accession: A94410
 A:Molecule type: protein
 A:Residues: 75-100 <KE2>
 R:Regier, G.W.; van Rietschoten, J.; Green, E.; Niall, H.D.; Keutmann, H.T.; Parsons, J.
 Hoppe-Seyler's Z. Physiol. Chem. 355, 415-421, 1974
 A:Title: Solid-phase synthesis of the biologically active N-terminal 1-34 peptide of human parathyroid hormone.
 A:Reference number: A91660; MUID:75059220; PMID:474131
 A:Contents: annotation; synthesis of residues 32-65
 A:Note: the biologically active amino-terminal 34 residues of parathyroid hormone were synthesized by solid-phase methods and characterized by biological assays. The sequence of the peptide at renal adenylate cyclase assay and with the bovine hormone's active region in the child R:Andreatta, R.H.; Hartmann, A.; Joehl, A.; Kamber, B.; Maier, R.; Riniker, B.; Rittel, Helv. Chim. Acta 56, 470-473, 1973
 A:Title: Synthese der Sequenz 1-34 von menschlichem Parat-hormon.
 A:Reference number: A91635; MUID:73227467; PMID:4721748
 A:Contents: annotation; synthesis of residues 32-65
 A:Note: the amino-terminal 34 residues of the parathyroid hormone sequence as determined into thyroparathyroidectomized rats caused a distinct increase in plasma calcium level
 R:Hendy, G.N.; Kronenberg, H.M.; Potts, J.T.
 Proc. Natl. Acad. Sci. U.S.A. 78, 7365-7369, 1981
 A:Title: Nucleotide sequence of cloned cDNAs encoding human preproparathyroid hormone.
 A:Reference number: I38342; MUID:82150870; PMID:6950381
 A:Accession: I38342
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-115 <RES>
 A:Cross-references: EMBL:V00597; NID:937143; PIDN:CAA23843.1; PID:937144
 C:Genetics:
 A:Gene: GDB:PTH
 A:Cross-references: GDB:119522; OMIM:168450
 A:Map position: 11p15.2-11p15.1
 A:Introns: 29/2
 A:Note: the first intron occurs before the initiator codon
 C:Function:
 A:Description: factor in homeostatic control of plasma calcium and phosphate; released by parathyroid gland; counter to calcitonin
 C:Superfamily: parathyroid hormone; parathyroid hormone homology
 C:Keywords: calcium; hormone; parathyroid gland; plasma
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:26-31/Domain: propeptide #status experimental <PRO>
 F:30-64/Domain: parathyroid hormone homology <PTH>
 F:32-115/Product: parathyroid hormone #status experimental <MAT>
 Query Match 98.8%; Score 417; DB 1; Length 115;
 Best Local Similarity 98.8%; Pred. No. 5.4e-37;
 Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VSEIQMHNLGKHLNSMERVWLKKLDVHNFVALGAPLAPRDAGSQRPKKEDNVLYE 60
 |||||
 Db 33 VSEIQMHNLGKHLNSMERVWLKKLDVHNFVALGAPLAPRDAGSQRPKKEDNVLYE 92
 QY 61 SHEKSLGEAKADVNVLTKAKSQ 83
 |||||
 Db 93 SHEKSLGEAKADVNVLTKAKSQ 115

RESULT 2

JC4202

parathyroid hormone precursor - dog

C:Species: Canis lupus familiaris (dog)

C:Date: 10-Sep-1995 #sequence_revision 27-Oct-1995 #text_change 16-Jul-1999

R:Rosol, T.J.; Steinmeyer, C.L.; McCauley, L.K.; Groene, A.; Dewille, J.W.; Cai

Gene 160, 241-243, 1995

A:Title: Sequences of the cDNAs encoding canine parathyroid hormone-related pr

A:Reference number: JC4201; MUID:95369696; PMID:7642102

A:Accession: JC4202

A:Molecule type: mRNA

A:Residues: 1-115 <ROS>

A:Cross-references: GB:U15662; NID:9558915; PIDN:AAA82584.1; PID:9558916

C:Superfamily: parathyroid hormone; parathyroid hormone homology

C:Keywords: hormone

F:1-31/Domain: signal sequence #status predicted <SIG>

F:30-64/Domain: parathyroid hormone homology <PTH>

F:32-115/Product: parathyroid hormone #status predicted <MAT>

Query Match 86.7%; Score 366; DB 2; Length 115;
 Best Local Similarity 86.7%; Pred. No. 1.3e-31;
 Matches 72; Conservative 6; Mismatches 5; Indels 0; Gaps 0;QY 1 VSEIQMHNLGKHLNSMERVWLKKLDVHNFVALGAPLAPRDAGSQRPKKEDNVLYE 60
 |||||
 Db 33 VSEIQMHNLGKHLNSMERVWLKKLDVHNFVALGAPLAPRDAGSQRPKKEDNVLYE 92
 QY 61 SHEKSLGEAKADVNVLTKAKSQ 83
 |||||
 Db 93 SYOKSLGEADKADVNVLTKAKSQ 115

RESULT 3

PTB0

parathyroid hormone precursor - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 18-Jun-1999

C:Accession: A24949; A93835; A93793; A91648; A93773; I45975; I45976; A01534

R:Weaver, C.A.; Gordon, D.F.; Kissil, M.S.; Mead, D.A.; Kemper, B.

Gene 28, 319-329, 1984

A:Title: Isolation and complete nucleotide sequence of the gene for bovine para

A:Reference number: A24949; MUID:84262483; PMID:6086460

A:Accession: A24949

A:Molecule type: DNA

A:Residues: 1-115 <WEA>

A:Cross-references: GB:K01938

R:Kronenberg, H.M.; McDevitt, B.E.; Majzoub, J.A.; Nathans, J.; Sharp, P.A.;

Proc. Natl. Acad. Sci. U.S.A. 76, 4981-4985, 1979

A:Title: Cloning and nucleotide sequence of DNA coding for bovine preproparathy

A:Reference number: A93835; MUID:80056617; PMID:388425

A:Accession: A93835

A:Molecule type: DNA

A:Residues: 1-115 <KRO>

A:Cross-references: GB:V00106; GB:J00023; NID:984; PIDN:CAA23439.1; PID:985

A:Note: The authors translated the codon GAA for residue 50 as Gly

R:Hamilton, J.W.; Niall, H.D.; Jacobs, J.W.; Keutmann, H.T.; Potts Jr., J.T.;

Proc. Natl. Acad. Sci. U.S.A. 71, 653-656, 1974

A:Title: The N-terminal amino-acid sequence of bovine parathyroid hormone.

A:Reference number: A93793; MUID:74142666; PMID:4522780

A:Accession: A93793

A:Molecule type: protein

A:Residues: 26-115 <HAM>

R:Niall, H.D.; Keutmann, H.T.; Sauer, R.; Hogan, M.L.; Dawson, B.F.; Aurbach,

Hoppe-Seyler's Z. Physiol. Chem. 351, 1586-1588, 1970

A:Title: The amino acid sequence of bovine parathyroid hormone I.

A:Reference number: A91648; MUID:71076162; PMID:5531031

A:Accession: A91648

A:Molecule type: protein

A:Residues: 32-115 <NIA>

R:Brewer Jr., H.B.; Ronan, R.

Proc. Natl. Acad. Sci. U.S.A. 67, 1862-1869, 1970

A:Title: Bovine parathyroid hormone: amino acid sequence.
 A:Reference number: A93773; MUID:71063634; PMID:5275384
 A:Accession: A93773
 A:Molecule type: protein
 A:Residues: 32-115 <BRE>
 R:Potts Jr., J.T.; Tregear, G.W.; Keutmann, H.T.; Niall, H.D.; Sauer, R.; Deftos, L.J.; Proc. Natl. Acad. Sci. U.S.A. 68, 63-67, 1971
 A:Title: Synthesis of a biologically active N-terminal tetraoctapeptide of parathyroid hormone.
 A:Reference number: A93776; MUID:71091588; PMID:4322265
 A:Contents: annotation; synthesis of residues 32-65
 A:Note: the synthetic peptide was active in vivo and in vitro
 R:Brewer Jr., H.B.; Fairwell, T.; Rittel, W.; Littledike, T.; Arnaud, C.D. Am. J. Med. 56, 759-766, 1974
 A:Title: Recent studies on the chemistry of human, bovine and porcine parathyroid hormone.
 A:Reference number: A90030; MUID:74173303; PMID:4598526
 A:Contents: annotation
 R:Weaver, C.A.; Gordon, D.F. Proc. Natl. Acad. Sci. U.S.A. 78, 4073-4077, 1981
 A:Title: Introduction by molecular cloning of artifactual inverted sequences at the 5' end of the parathyroid hormone gene.
 A:Reference number: A45975; MUID:82037785; PMID:6170060
 A:Accession: I45975
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-115 <WE2>
 A:Cross-references: GB:J00024; NID:g163642; PIDN:AAA30747.1; PID:g163643
 R:Weaver, C.A.; Gordon, D.F. Mol. Cell. Endocrinol. 28, 411-424, 1982
 A:Title: Nucleotide sequence of bovine parathyroid hormone messenger RNA.
 A:Reference number: I45976; MUID:83105964; PMID:6185374
 A:Accession: I45976
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-115 <WE3>
 A:Cross-references: GB:M25082; NID:g163644; PIDN:AAA30748.1; PID:g163645
 C:Genetics:
 A:Gene: PTH
 A:Introns: 29/2
 C:Superfamily: parathyroid hormone; parathyroid hormone homology
 C:Keywords: hormone
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:26-31/Domain: propeptide #status experimental <PMAT>
 F:30-64/Domain: parathyroid hormone homology <PRO>
 F:32-115/Product: parathyroid hormone #status experimental <MAT>
 Query Match 85.1%; Score 359; DB 1; Length 115;
 Best Local Similarity 85.5%; Pred. No. 7.2e-31;
 Matches 71; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
 QY 1 VSEIQMHNGLKHLNLSMERVEWLRKLLQDVHNFVALGAPLAPRDAGSQRPKKEDNVLVE 60
 DB 33 VSEIQPMHNLGKHLNLSMERVEWLRKLLQDVHNFVALGASVAYRDGSSQRPKKEDNVLVE 92
 QY 61 SHEKSLGEANKADVNVLTAKSQ 83
 DB 93 SHQKSLGEADKADVDVLIKAPQ 115
 RESULT 4
 PTPG
 parathyroid hormone precursor - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 24-Apr-1984 #sequence_revision 12-Apr-1996 #text_change 18-Jun-1999
 C:Accession: B26806; A90390; A90376; A01535
 R:Schmelzer, H.J.; Gross, G.; Widera, G.; Mayer, H. Nucleic Acids Res. 15, 6740, 1987
 A:Title: Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid hormone.
 A:Reference number: A26806; MUID:87316938; PMID:3628009
 A:Accession: B26806
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-115 <SCH>
 A:Cross-references: GB:X05722; GB:Y00409; NID:g1838; PIDN:CAA29193.1; PID:g1839

R:Chu, L.L.H.; Huang, W.Y.; Littledike, E.T.; Hamilton, J.W.; Cohn, D.V. Biochemistry 14, 3631-3635, 1975
 A:Title: Porcine parathyroid hormone. Identification, biosynthesis, and partial amino acid sequence.
 A:Reference number: A90390; MUID:76018954; PMID:1164500
 A:Accession: A90390
 A:Molecule type: protein
 A:Residues: 26-115 <CHU>
 R:Sauer, R.T.; Niall, H.D.; Hogan, M.L.; Keutmann, H.T.; O'Riordan, J.L.H.; Potts, J. Biochemistry 13, 1994-1999, 1974
 A:Title: The amino acid sequence of porcine parathyroid hormone.
 A:Reference number: A90376; MUID:74253317; PMID:4840833
 A:Accession: A90376
 A:Molecule type: protein
 A:Residues: 32-109 <SNU>
 R:Brewer Jr., H.B.; Fairwell, T.; Rittel, W.; Littledike, T.; Arnaud, C.D. Am. J. Med. 56, 759-766, 1974
 A:Title: Recent studies on the chemistry of human, bovine and porcine parathyroid hormone.
 A:Reference number: A90030; MUID:74173303; PMID:4598526
 A:Contents: annotation
 C:Superfamily: parathyroid hormone; parathyroid hormone homology
 C:Keywords: calcium; hormone; parathyroid gland
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:26-31/Domain: propeptide #status experimental <PRO>
 F:30-64/Domain: parathyroid hormone homology <PTH>
 F:32-115/Product: parathyroid hormone #status experimental <MAT>
 Query Match 84.1%; Score 355; DB 1; Length 115;
 Best Local Similarity 84.3%; Pred. No. 1.9e-30;
 Matches 70; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
 QY 1 VSEIQMHNGLKHLNLSMERVEWLRKLLQDVHNFVALGAPLAPRDAGSQRPKKEDNVLVE 60
 DB 33 VSEIQMHNGLKHLNLSMERVEWLRKLLQDVHNFVALGASVAYRDGSSQRPKKEDNVLVE 92
 QY 61 SHEKSLGEANKADVNVLTAKSQ 83
 DB 93 SHQKSLGEADKADVDVLIKAPQ 115
 RESULT 5
 A05091
 parathyroid hormone precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 16-Jul-1999
 C:Accession: A05091; A26806
 R:Heinrich, G.; Kronenberg, H.M.; Potts Jr., J.T.; Habener, J.F. J. Biol. Chem. 259, 3320-3329, 1984
 A:Reference number: A05091; MUID:84135846; PMID:6321505
 A:Accession: A05091
 A:Molecule type: DNA
 A:Residues: 1-115 <HE1>
 A:Cross-references: GB:K01268; NID:g206483; PIDN:AAA41979.1; PID:g206485
 A:Note: the authors translated the codon GAA for residue 87 as Asp
 R:Schmelzer, H.J.; Gross, G.; Widera, G.; Mayer, H. Nucleic Acids Res. 15, 6740, 1987
 A:Title: Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid hormone.
 A:Reference number: A26806; MUID:87316938; PMID:3628009
 A:Accession: A26806
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-115 <SCH>
 A:Cross-references: GB:X05721; GB:Y00409; NID:g56002; PIDN:CAA29192.1; PID:g56003
 C:Genetics:
 A:Introns: 29/3
 C:Superfamily: parathyroid hormone; parathyroid hormone homology
 F:30-64/Domain: parathyroid hormone homology <PTH>
 Query Match 73.7%; Score 311; DB 2; Length 115;
 Best Local Similarity 72.3%; Pred. No. 8.4e-26;
 Matches 60; Conservative 11; Mismatches 12; Indels 0; Gaps 0;
 QY 1 VSEIQMHNGLKHLNLSMERVEWLRKLLQDVHNFVALGAPLAPRDAGSQRPKKEDNVLVE 60

Db 33 VSEIQLMHNIGKHLASVERMQWLRLKLDQVHNFVSLGVMAAREGSYQRPTRKKEENVLVD 92

QY 61 SHEKSLGEANKADVNLTKAKSQ 83

Db 93 GNSKSLGEGKADVDVLTKAKSQ 115

RESULT 6

I51851
parathyroid hormone - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C:Accession: I51851
R:Schmelzer, H.
Adv. Gene Technol. 21, 228-229, 1984
A:Title: Nucleotide sequence of cloned cDNA encoding rat prepro parathyroid hormone.
A:Reference number: I51851
A:Accession: I51851
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-105 <RES>
A:Cross-references: GB:M54875; NID:g601932; PIDN:AAA57156.1; PID:g601933
C:Genetics:
A:Gene: PTH
C:Superfamily: parathyroid hormone; parathyroid hormone homology
F:20-54/Domain: parathyroid hormone homology <PTH>

Query Match 71.8%; Score 303; DB 2; Length 105;
Best Local Similarity 69.9%; Pred. No. 5.3e-25;
Matches 58; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

QY 1 VSEIQLMHNIGKHLASVERMQWLRLKLDQVHNFVSLGVMAAREGSYQRPTRKKEENVLVD 60

Db 23 ISEIQLMHNIGKHLASVERMQWLRLKLDQVHNFVSLGVMAAREGSYQRPTRKKEENVLVD 82

QY 61 SHEKSLGEANKADVNLTKAKSQ 83

Db 83 GNSKSLGEGKADVDVLTKAKSQ 105

RESULT 7

A34937
Parathyroid hormone precursor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 16-Jul-1999
C:Accession: A34937; I50411
R:Russell, J.; Sherwood, L.M.
Mol. Endocrinol. 3, 325-331, 1989
A:Title: Nucleotide sequence of the DNA complementary to avian (chicken) preproparathyroid hormone.
A:Reference number: A34937; MUID:89219100; PMID:2710135
A:Accession: A34937
A:Molecule type: mRNA
A:Residues: 1-119 <RUS>
A:Cross-references: GB:M31604; NID:g212767; PIDN:AAA49093.1; PID:g212768
R:Khosla, S.; Demay, M.; Pines, M.; Hurwitz, S.; Potts, J.T.
J. Bone Miner. Res. 3, 689-698, 1988
A:Title: Nucleotide sequence of cloned cDNAs encoding chicken preproparathyroid hormone.
A:Reference number: I50411; MUID:89284968; PMID:3251402
A:Accession: I50411
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-119 <KHO>
A:Cross-references: NID:g212591; PIDN:AA02866.1; PID:g212592
C:Superfamily: parathyroid hormone; parathyroid hormone homology.
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-31/Domain: propeptide #status predicted <PRO>
F:30-64/Domain: parathyroid hormone homology <PTH>
F:32-119/Product: parathyroid hormone #status predicted <MAT>

Query Match 41.4%; Score 174.5; DB 2; Length 119;
Best Local Similarity 44.7%; Pred. No. 2.3e-11;
Matches 42; Conservative 14; Mismatches 17; Indels 21; Gaps 2;

QY 1 VSEIQLMHNIGKHLASVERMQWLRLKLDQVHNFVSLGVMAAREGSYQRPTRKKEENVLVD 60
Db 33 VSEIQLMHNIGKHLASVERMQWLRLKLDQVHNFVSLGVMAAREGSYQRPTRKKEENVLVD 84
QY 61 SHEKSLGEANKADVNLTKAKSQ 81
Db 85 IRRNRLLEHLRAAVQKSDLDKAYMNVLFKTK 118

RESULT 8

G89813
DNA polymerase III gamma and tau subunits [imported] - Staphylococcus aureus (s)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: G89813
R:Kuroda, M.; Ohka, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, M.; A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimura, A.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: G89813
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-565 <KUR>
A:Cross-references: GB:BA000018; PID:gl3700368; PIDN:BA041666.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: dnaX
C:Superfamily: DNA-directed DNA polymerase III gamma chain

Query Match 17.3%; Score 73; DB 2; Length 565;
Best Local Similarity 29.4%; Pred. No. 7.1;
Matches 20; Conservative 15; Mismatches 23; Indels 10; Gaps 2;

QY 14 LNSMERVEWLRLKLDQVHNFVSLGVMAAREGSYQRPTRKKEENVLVD 69

Db 376 LORMEQLE-----QELTKAQGVAPAKSKKPKARGIKSNKAFSMOQIAKVLDKA 429

QY 70 NKADVNL 77

Db 430 NKADIKLL 437

RESULT 9

F72408
leucine-tRNA ligase (EC 6.1.1.4) - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 03-Jun-2002
C:Accession: F72408
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Garret, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richard, C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from g
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: F72408
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-824 <ARN>
A:Cross-references: GB:AE001702; GB:AE000512; NID:g4980662; PIDN:AA035261.1; P
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM0168
C:Superfamily: leucine-tRNA ligase
C:Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 17.2%; Score 72.5; DB 2; Length 824;
Best Local Similarity 23.3%; Pred. No. 12;
Matches 21; Conservative 25; Mismatches 25; Indels 19; Gaps 4;
QY 4 IQLMHNIGKHLASVERMQWLRLKLDQVHNFVSLGVMAAREGSYQRPTRKKEENVLVD 55

QY	13	HLSMSERVEWRKKLQDVHN-FVALCAPLRPDAGSQRPKRKEDNVLVSHESKSLGEANK	71
		:::: ::: ::: ::: ::: ::: ::: ::: :::	:
D6	1179	NNNSTERISFLOEKLEIKRYMSLKSEVATIDRRKRUKKKDREV---SHAGASSSSAS	1235

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2003, 08:08:56 ; Search time 59.4627 Seconds
(without alignments)
221.556 Million cell updates/sec

Title: US-09-928-048A-4
Perfect score: 422
Sequence: 1 VSEIQLMHLNGLHLSMERY.....KSLGEANKADNVLTAKSQ 83

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03:*

1:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
6:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
7:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
8:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
9:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
10:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
11:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
12:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
13:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
14:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
15:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
16:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
17:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
18:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
19:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
24:	/SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	422	100.0	83	24	ABG74230 Human parathyroid
2	422	100.0	84	21	ABG7464 Amino acid sequenc
3	422	100.0	84	24	ABG74234 Human full length
4	418	99.1	82	21	ABG7465 Amino acid sequenc
5	418	99.1	82	24	ABG74231 Human parathyroid
6	417	98.8	84	13	AA23790 Parathyroid hormon
7	417	98.8	84	13	AA25571 Human PTH encoded
8	417	98.8	84	14	AA242067 Human parathyroid
9	417	98.8	84	17	AAW29420 Human parathyroid

10	417	98.8	84	17	AA98954 Target peptide (PT
11	417	98.8	84	18	AAW25687 Human parathyroid
12	417	98.8	84	20	AAV02577 Human parathyroid
13	417	98.8	84	22	ABG91082 Parathyroid hormon
14	417	98.8	84	23	ABG71472 Human parathyroxin
15	417	98.8	84	23	AAE23726 Human parathyroid
16	417	98.8	84	23	ABH08594 Human parathyroid
17	417	98.8	84	23	AAE18392 Human PTH peptide
18	417	98.8	84	23	AAE14316 Salmon calcitonin
19	417	98.8	84	23	AAU73022 Parathyroid hormon
20	417	98.8	84	24	ABG76363 Human parathyroid
21	417	98.8	84	24	ABG72601 Human bioactive pa
22	417	98.8	115	5	AA40251 Protein sequence i
23	417	98.8	115	9	AA80305 Sequence of human
24	417	98.8	115	9	AA80275 Sequence of human
25	417	98.8	115	16	AA875693 Human prepro-PTH.
26	417	98.8	84	13	AA828846 Oxidation resistan
27	417	98.8	84	13	AA828848 Oxidation resistan
28	417	98.8	84	14	AA830857 Leu18 hPTH mutein.
29	413	97.9	84	14	AA842068 Stability-enhanced
30	412	97.6	84	14	AA830856 Cys35 hPTH mutein.
31	412	97.6	84	14	AA842070 Stability-enhanced
32	412	97.6	84	17	AA89448 Human parathyroid
33	412	97.6	84	23	ABJ05329 Human PTH(1-84) pe
34	411	97.4	84	13	AA828845 Oxidation resistan
35	411	97.4	84	13	AA828847 Oxidation resistan
36	411	97.4	84	13	AA829562 Oxidation resistan
37	411	97.4	84	14	AA842071 Stability-enhanced
38	411	97.4	84	15	AA849892 Sequence of varian
39	411	97.4	84	15	AA849893 Sequence of varian
40	411	97.4	84	15	AA849694 Sequence of varian
41	410	97.2	84	13	AA829564 Oxidation resistan
42	410	97.2	84	13	AA829565 Oxidation resistan
43	410	97.2	84	14	AA842069 Stability-enhanced
44	410	97.2	84	15	AA849896 Sequence of varian
45	409	96.9	81	14	AA830854 hPTH mutein lackin

ALIGNMENTS

RESULT 1
ABG74230
ID ABG74230 standard; peptide; 83 AA.
XX AC ABG74230;
XX AC
XX 16-APR-2003 (first entry)
XX DE Human parathyroid hormone-based CIP, PTH2-84.
XX DE Parathyroid hormone; PTH; cyclase activating parathyroid hormone;
KW KW CAP; cyclase inhibiting parathyroid hormone; CIP; osteoporosis;
KW KW hypercalcaemia; osteosarcoma; extracellular calcium; PTH2-84.
XX OS Homo sapiens.
XX PN US2002160945-A1.
XX PD 31-OCT-2002.
XX PF 10-AUG-2001; 2001US-0928047.
XX PR 10-AUG-2000; 2000US-224446P.
XX PA (CANT/) CANTOR T L.
XX PI Cantor TL;
XX DR WPI; 2003-209227/20.
XX PT Treating a patient having osteoporosis and is being administered
PT cyclase activating parathyroid hormone or its analogue comprises

PT administering a cyclase inhibiting parathyroid hormone peptide -
 PS Claim 1; Page 3; 8pp; English.
 XX The invention relates to treating a patient having osteoporosis
 CC comprising administering a cyclase inhibiting parathyroid hormone peptide
 CC (CIP) or its conservatively substituted variant exhibiting a parathyroid
 CC hormone (PTH, which regulates extracellular calcium levels) antagonist
 CC activity to reduce the occurrence of hypercalcaemia or osteosarcoma in
 CC the patient resulting from the administration of CAP. The peptide
 CC comprises PTH2-84, PTH34-84, PTH3-84 and PTH28-84 (appearing as ABG74230
 CC -ABG74233). The present sequence is the CIP PTH2-84.
 XX
 XX Sequence 83 AA;
 SQ
 Query Match 100.0%; Score 422; DB 24; Length 83;
 Best Local Similarity 100.0%; Pred. No. 5.7e-42;
 Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VSEIQLMHNKLGKHLNSMERVEWLRKKLDVHNFVALGAPLAPRDAGSQRPKKEDNVLVE 60
 DB 1 VSEIQLMHNKLGKHLNSMERVEWLRKKLDVHNFVALGAPLAPRDAGSQRPKKEDNVLVE 60
 QY 61 SHEKSLGEANKADVNLTKAQSO 83
 DB 61 SHEKSLGEANKADVNLTKAQSO 83
 RESULT 2
 AAB07464
 ID AAB07464 standard; protein; 84 AA.
 AC AAB07464;
 XX
 DT 20-OCT-2000 (first entry)
 XX
 DE Amino acid sequence of human parathyroid hormone.
 XX
 KW Human; parathyroid hormone; PTH; hyperparathyroidism; bone disease.
 XX
 OS Homo sapiens.
 XX
 PN WO2000042437-A1.
 XX
 PD 20-JUL-2000.
 XX
 PF 13-JAN-2000; 2000WO-US00855.
 XX
 PR 14-JAN-1999; 99US-0231422.
 XX
 PR 26-JUN-1999; 99US-0344639.
 XX
 PA (SCAN-) SCANTIBODIES LAB INC.
 XX
 DR WPI; 2000-476147/41.
 XX
 PT Differentiating between normal parathyroid function and
 PT hyperparathyroidism comprises determining and comparing whole
 PT parathyroid hormone, parathyroid hormone inhibitory peptide fragment
 PT and/or total parathyroid hormone levels
 XX
 PS Disclosure; Fig 1; 46pp; English.
 XX
 CC The present sequence represents a human parathyroid hormone (PTH).
 CC Fragments of PTH function as PTH antagonists. The specification
 CC describes a method for differentiating between a person having
 CC substantially normal parathyroid function and having hyperparathyroidism.
 CC The method comprises determining and comparing at least two of the
 CC following parameters: whole parathyroid hormone level, parathyroid
 CC hormone inhibitory peptide fragment level and total parathyroid hormone
 CC level. The method is used for monitoring (treatments of) parathyroid
 CC related bone disease and the effects of therapeutic treatment for
 CC hyperparathyroidism.
 XX

SQ Sequence 84 AA;
 Query Match 100.0%; Score 422; DB 21; Length 84;
 Best Local Similarity 100.0%; Pred. No. 5.7e-42;
 Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VSEIQLMHNKLGKHLNSMERVEWLRKKLDVHNFVALGAPLAPRDAGSQRPKKEDNVLVE 60
 DB 2 VSEIQLMHNKLGKHLNSMERVEWLRKKLDVHNFVALGAPLAPRDAGSQRPKKEDNVLVE 61
 QY 61 SHEKSLGEANKADVNLTKAQSO 83
 DB 62 SHEKSLGEANKADVNLTKAQSO 84
 RESULT 3
 ABG74234
 ID ABG74234 standard; peptide; 84 AA.
 XX
 AC ABG74234;
 XX
 DT 16-APR-2003 (first entry)
 XX
 DE Human full length parathyroid hormone.
 XX
 KW Parathyroid hormone; PTH; cyclase activating parathyroid hormone;
 KW CAP; cyclase inhibiting parathyroid hormone; CIP; osteoporosis;
 KW hypercalcaemia; osteosarcoma; extracellular calcium.
 XX
 OS Homo sapiens.
 XX
 PN US2002160945-A1.
 XX
 PD 31-OCT-2002.
 XX
 PF 10-AUG-2001; 2001US-0928047.
 XX
 PR 10-AUG-2000; 2000US-224446P.
 XX
 PA (CANT/) CANTOR T L.
 XX
 PI Cantor TL;
 XX
 DR WPI; 2003-209227/20.
 XX
 PT Treating a patient having osteoporosis and is being administered
 PT cyclase activating parathyroid hormone or its analogue comprises
 PT administering a cyclase inhibiting parathyroid hormone peptide -
 PS Disclosure; Fig 1; 8pp; English.
 XX
 CC The invention relates to treating a patient having osteoporosis
 CC comprising administering a cyclase inhibiting parathyroid hormone peptide
 CC (CIP) or its conservatively substituted variant exhibiting a parathyroid
 CC hormone (PTH, which regulates extracellular calcium levels) antagonist
 CC activity to reduce the occurrence of hypercalcaemia or osteosarcoma in
 CC the patient resulting from the administration of CAP. The peptide
 CC comprises PTH2-84, PTH34-84, PTH3-84 and PTH28-84 (appearing as ABG74230
 CC -ABG74233). The present sequence is full length human PTH, the sequence
 CC upon which the CIP peptides are based.
 XX
 XX Sequence 84 AA;
 Query Match 100.0%; Score 422; DB 24; Length 84;
 Best Local Similarity 100.0%; Pred. No. 5.7e-42;
 Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VSEIQLMHNKLGKHLNSMERVEWLRKKLDVHNFVALGAPLAPRDAGSQRPKKEDNVLVE 60
 DB 2 VSEIQLMHNKLGKHLNSMERVEWLRKKLDVHNFVALGAPLAPRDAGSQRPKKEDNVLVE 61
 QY 61 SHEKSLGEANKADVNLTKAQSO 83
 DB 61 SHEKSLGEANKADVNLTKAQSO 83

Db 62 SHEKSLGEANKADVNVLTKAKSQ 84

RESULT 4
AAB07465
ID AAB07465 standard; protein; 82 AA.
XX AC AAB07465;
XX DT 20-OCT-2000 (first entry)
XX DE Amino acid sequence of human parathyroid hormone antagonist.
XX KW Human; parathyroid hormone; PTH; hyperparathyroidism; bone disease.
XX OS Homo sapiens.
XX PN WO2000042437-A1.
XX PD 20-JUL-2000.
XX 13-JAN-2000; 2000WO-US00855.
XX PF 14-JAN-1999; 99US-0231422.
XX PR 26-JUN-1999; 99US-0344639.
XX PA (SCAN-) SCANTIBODIES LAB INC.
XX DR WPI; 2000-476147/41.
XX PT Differentiating between normal parathyroid function and
PT hyperparathyroidism comprises determining and comparing whole
PT parathyroid hormone, parathyroid hormone inhibitory peptide fragment
PT and/or total parathyroid hormone levels -
XX PS Disclosure; Page 42-43; 46pp; English.
XX CC The present sequence represents a fragment of human parathyroid
CC hormone (PTH), comprising residues 3-84, which functions as a PTH
CC antagonist. The specification describes a method for differentiating
CC between a person having substantially normal parathyroid function
CC and having hyperparathyroidism. The method comprises determining and
CC comparing at least two of the following parameters: whole parathyroid
CC hormone level, parathyroid hormone inhibitory peptide fragment level
CC and total parathyroid hormone level. The method is used for monitoring
CC (treatments of) parathyroid related bone disease and the effects of
CC therapeutic treatment for hyperparathyroidism.
XX SQ Sequence 82 AA;
Query Match 99.1%; Score 418; DB 21; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.6e-41;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SETQLMHNLGKHLNSMERVWLKQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVES 61
Db 1 SETQLMHNLGKHLNSMERVWLKQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVES 60
QY 62 HEKSLGEANKADVNVLTKAKSQ 83
Db 61 HEKSLGEANKADVNVLTKAKSQ 82
RESULT 5
ABG74231
ID ABG74231 standard; peptide; 82 AA.
XX AC ABG74231;
XX DT 16-APR-2003 (first entry)
XX DE Human parathyroid hormone-based CIP, PTH34-84.
XX PR 20-MAR-1991; 91JP-0056434.

KW Parathyroid hormone; PTH; cyclase activating parathyroid hormone;
KW CAP; cyclase inhibiting parathyroid hormone; CIP; osteoporosis;
XX hypercalcaemia; osteosarcoma; extracellular calcium; PTH34-84.
XX OS Homo sapiens.
XX PN US2002160945-A1.
XX PD 31-OCT-2002.
XX 10-AUG-2001; 2001US-0928047.
XX PF 10-AUG-2000; 2000US-224446P.
XX PR (CANT/) CANTOR T L.
XX PA Cantor TL;
XX PI WPI; 2003-209227/20.
XX DR Treating a patient having osteoporosis and is being administered
XX PT cyclase activating parathyroid hormone or its analogue comprises
XX PT administering a cyclase inhibiting parathyroid hormone peptide -
XX PS Claim 1; Page 3; 8pp; English.
XX CC The invention relates to treating a patient having osteoporosis
XX CC comprising administering a cyclase inhibiting parathyroid hormone peptide
XX CC (CIP) or its conservatively substituted variant exhibiting a parathyroid
XX CC hormone (PTH), which regulates extracellular calcium levels) antagonist
XX CC activity to reduce the occurrence of hypercalcaemia or osteosarcoma in
XX CC the patient resulting from the administration of CAP. The peptide
XX CC comprises PTH2-84, PTH34-84, PTH3-84 and PTH28-84 (appearing as ABG74230
XX CC -ABG74233). The present sequence is the CIP PTH34-84.
XX SQ Sequence 82 AA;
Query Match 99.1%; Score 418; DB 24; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.6e-41;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SETQLMHNLGKHLNSMERVWLKQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVES 61
Db 1 SETQLMHNLGKHLNSMERVWLKQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVES 60
QY 62 HEKSLGEANKADVNVLTKAKSQ 83
Db 61 HEKSLGEANKADVNVLTKAKSQ 82
RESULT 6
AAR23790
ID AAR23790 standard; Protein; 84 AA.
XX AC AAR23790;
XX DT 03-NOV-1992 (first entry)
XX DE Parathyroid hormone gene product.
XX KW hPTH; hypoparathyroidism; osteoporosis.
XX OS Synthetic.
XX PN EP483509-A.
XX PD 06-MAY-1992.
XX PF 25-SEP-1991; 91EP-0116281.
XX PR 28-SEP-1990; 90JP-0257491.
XX PR 20-MAR-1991; 91JP-0056434.

PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Fukuda T, Oshikazu Y, Yamada T;
 XX
 DR WPI; 1992-152248/19.
 XX
 DR N-PSDB; AAQ24478.
 XX
 PT Synthetic gene encoding human parathyroid hormone - formed by
 PT ligating oligo-nucleotide(s) and expressed at high yield in E
 PT coli
 XX
 PS Disclosure; Page 21; 33pp; English.
 XX
 CC The human parathyroid hormone (hPTH) sequence given is the product of
 CC a synthetic gene which corresponds to the amino acid sequence of hPTH.
 CC The DNA sequence was produced by enzymatically ligating
 CC oligodeoxynucleotides. hPTH is an important regulator of calcium
 CC metabolism and has clinical applicns. to diseases such as
 CC hypoparathyroidism and osteoporosis. This hPTH can be used as a
 CC therapeutic agent or to study the biological role of hPTH in vivo.
 XX
 SQ Sequence 84 AA;
 Query Match 98.8%; Score 417; DB 13; Length 84;
 Best Local Similarity 98.8%; Pred. No. 2.2e-41;
 Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VSEIQLMHNIGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE 60
 DB 2 VSEIQLMHNIGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE 61
 QY 61 SHEKSLGEANKADYNVLTAKSQ 83
 DB 62 SHEKSLGEADKADYNVLTAKSQ 84
 RESULT 7
 AAR25571
 ID AAR25571 standard; Protein; 84 AA.
 XX
 AC AAR25571;
 XX
 DT 25-MAR-2003 (updated)
 DT 13-JAN-1993 (first entry)
 XX
 DE Human PTH encoded by px.
 XX
 KW Parathyroid; hormone; osteoporosis; psoriasis; oxidation;
 KW resistance.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 8 /note= "see CC"
 FT Misc-difference 18 /note= "see CC"
 FT
 XX
 PN WO9211286-A1.
 XX
 PD 09-JUL-1992.
 XX
 PF 18-DEC-1991; 91WO-CA00451.
 XX
 PR 21-DEC-1990; 90US-0630969.
 PR 13-DEC-1991; 91US-0806271.
 XX
 PA (ALIX) ALLELIX BIOPHARMACEUTICALS INC.
 PA (GLAX) GLAXO CANADA INC.
 XX
 PI Bozzatto RP, Kronis KA;
 XX
 DR WPI; 1992-250028/30.
 XX

DR N-PSDB; AAQ26498.
 XX
 PT New oxidn. resistant variants of parathyroid hormone - used for
 PT treating osteoporosis, psoriasis and cardiovascular disorders
 XX
 PS Disclosure; Fig 1; 40pp; English.
 XX
 CC Variants of PTH exhibiting PTH activity and reduced sensitivity
 CC to oxidation are obtained by replacing at least one Met residue in
 CC PTH (positions 8 and 18) with a genetically encoded amino acid,
 CC other than Met and Cys.
 CC The Met amino acids are indicated in the Features Table.
 CC The variant may be obtd. using recombinant technique, and may be
 CC used for treating osteoporosis, other bone-related disorders,
 CC psoriasis and cardiovascular disorders.
 CC Human PTH refers to the mature form of the hormone, which consists
 CC of 84 amino acids arranged in the sequence reported by Kimura et al,
 CC 1983, Biochem. Biophys. Res. Comm., 114(2):493.
 CC Examples of variants are given in AAR2845-48 and AAR29561-69.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 84 AA;
 Query Match 98.8%; Score 417; DB 13; Length 84;
 Best Local Similarity 98.8%; Pred. No. 2.2e-41;
 Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VSEIQLMHNIGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE 60
 DB 2 VSEIQLMHNIGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE 61
 QY 61 SHEKSLGEANKADYNVLTAKSQ 83
 DB 62 SHEKSLGEADKADYNVLTAKSQ 84
 RESULT 8
 AAR42067
 ID AAR42067 standard; Protein; 84 AA.
 XX
 AC AAR42067;
 XX
 DT 25-MAR-2003 (updated)
 DT 05-MAY-1994 (first entry)
 XX
 DE Human parathyroid hormone.
 XX
 KW PTH; hPTH; stability-enhanced; mutant; resistance; proteolytic;
 KW enzymes; osteoporosis; bone-related disorders.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 25...27
 FT /note= "ArgLysLys which may be mutated"
 XX
 PN WO9320203-A2.
 XX
 PD 14-OCT-1993.
 XX
 PF 31-MAR-1993; 93WO-CA00136.
 XX
 PR 03-APR-1992; 92US-0863014.
 XX
 PA (ALLX) ALLELIX BIOPHARMACEUTICALS INC.
 PA (GLAX) GLAXO CANADA INC.
 XX
 PI Bozzatto RP, Kronis KA;
 XX
 DR WPI; 1993-336911/42.
 DR N-PSDB; AAQ49955.
 XX

PT New parathyroid hormone variants - having aminoacid replacements
PT at positions 25 to 27 to enhance resistance to proteolytic
XX enzymes
PS Disclosure; Fig 2; 44pp; English.
XX The sequence is that of human parathyroid hormone (hPTH) which
CC may be mutated in the region Arg25Lys26Lys27 to provide variants
CC with enhanced stability in the presence of proteolytic enzymes
CC such as trypsin.
CC (Updated on 25-MAR-2003 to correct PN field.)
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 84 AA;

Query Match 98.8%; Score 417; DB 14; Length 84;
Best Local Similarity 98.8%; Pred. No. 2.2e-41;
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNGLGKHLNSMERVEWLKRLQDVHNFVALGAPLAPRDAGSORPKKEDNVLVE 60
Db 2 VSEIQLMHNGLGKHLNSMERVEWLKRLQDVHNFVALGAPLAPRDAGSORPKKEDNVLVE 61

QY 61 SHEKSLGEANKADVNLTAKSQ 83
Db 62 SHEKSLGEADKADVNLTAKSQ 84

RESULT 9
AAW29420
ID AAW29420 standard; protein; 84 AA.
XX
AC AAW29420;
XX
XX
DT 25-MAR-2003 (updated)
DT 24-FEB-1998 (first entry)
XX
XX Human parathyroid hormone.
XX
XX Parathyroid hormone; PTH; osteoporosis; inhalation; pulmonary;
KW bone formation.
XX
XX Homo sapiens.
XX
XX WO9619206-A1.
XX
XX 27-JUN-1996.
XX
XX 08-DEC-1995; 95WO-SE01475.
XX
XX 12-JUL-1995; 95SE-0002576.
XX
XX 22-DEC-1994; 94SE-0004449.
XX
XX (ASTR) ASTRA AB.
XX
XX Baeckstroem K, Wallmark B;
XX
XX WPI; 1996-309285/31.
XX
XX Composition for administration by inhalation to treat osteoporosis
PT and stimulate bone formation - comprises parathyroid hormone in form
PT of dry powder mainly of particle size below 10 microns
XX
XX Claim 9; Pages 15-16; 25pp; English.
XX
XX The present sequence represents human parathyroid hormone which is used
CC in a new therapeutic preparation for the treatment of osteoporosis.
CC The active substance is in the form of a dry powder suitable for
CC inhalation, in which at least 50% of the dry powder consists of particles
CC of up to 10 microns in diameter or agglomerates of such particles.
CC Pulmonary administration of the parathyroid hormone is effective in the
CC stimulation of bone formation.
CC (Updated on 25-MAR-2003 to correct PI field.)
CC

XX Sequence 84 AA;

Query Match 98.8%; Score 417; DB 17; Length 84;
Best Local Similarity 98.8%; Pred. No. 2.2e-41;
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNGLGKHLNSMERVEWLKRLQDVHNFVALGAPLAPRDAGSORPKKEDNVLVE 60
Db 2 VSEIQLMHNGLGKHLNSMERVEWLKRLQDVHNFVALGAPLAPRDAGSORPKKEDNVLVE 61

QY 61 SHEKSLGEANKADVNLTAKSQ 83
Db 62 SHEKSLGEADKADVNLTAKSQ 84

RESULT 10
AAR98954
ID AAR98954 standard; peptide; 84 AA.
XX
AC AAR98954;
XX
DT 15-JAN-1997 (first entry)
XX
XX Target peptide (PTH(1-84)) used in fusion protein construct.
XX
KW Fusion protein construct; isolation; purification;
KW growth hormone releasing factor; glucagon-like peptide 1;
KW parathyroid hormone; inclusion body; carbonic anhydrase.
XX
XX OS Synthetic.
XX
XX WO9617942-A1.
XX
XX 13-JUN-1996.
XX
XX 07-DEC-1995; 95WO-US15800.
XX
XX 07-DEC-1994; 94US-0350530.
XX
XX (BION-) BIONEERASKA INC.
XX
XX De LA MOTTE RS, Henriksen DB, Holmquist B, Manning SD;
XX Partridge BE, Stout JS, Wagner FW;
XX
XX WPI; 1996-287186/29.
XX
XX Isolation and purific of peptide(s) from fusion protein constructs
PT - which include a carbonic anhydrase and a variable fused
PT polypeptide
XX
XX Claim 58; Page 49; 67pp; English.
XX
XX A new method for the isolation and/or purification of a recombinant
CC peptide employs a fusion protein construct (FPC) comprising a
CC carbonic anhydrase and a variable fused polypeptide containing a
CC target peptide. The method comprises precipitating either the FPC or
CC a fragment of the FPC including the carbonic anhydrase. An
CC alternative method of producing the peptide comprises expressing the
CC FPC as part of an inclusion body. The target peptides of the FPC are
CC derived from growth hormone releasing factor (GRF), glucagon-like
CC peptide 1 (GluP1) or parathyroid hormone (PTH). This sequence
CC corresponds to amino acids 1-84 of PTH.
XX
SQ Sequence 84 AA;

Query Match 98.8%; Score 417; DB 17; Length 84;
Best Local Similarity 98.8%; Pred. No. 2.2e-41;
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNGLGKHLNSMERVEWLKRLQDVHNFVALGAPLAPRDAGSORPKKEDNVLVE 60
Db 2 VSEIQLMHNGLGKHLNSMERVEWLKRLQDVHNFVALGAPLAPRDAGSORPKKEDNVLVE 61

QY 61 SHEKSLGEANKADYNVLTAKSQ 83
DB 62 SHEKSLGEADKADYNVLTAKSQ 84

RESULT 11

AAW25687
ID AAW25687 standard; Peptide; 84 AA.

XX AC AAW25687;

DT 14-APR-1998 (first entry)

DE Human parathyroid hormone peptide hPTH (residues 1-84).

KW Kex2 protease; derivative; cleave; yeast; enzyme; chimeric protein;
KW human; parathyroid hormone peptide; hPTH.

XX OS Homo sapiens.

FH Key Location/Qualifiers

FT Cleavage-site 43..44

FT /note= "cleaved by Kex2 protease"

FT Cleavage-site 51..52

FT /note= "cleaved by Kex2 protease"

XX EP794254-A2.

XX PN 10-SEP-1997.

XX PD 04-MAR-1997; 97EP-0301429.

XX PR 16-DEC-1996; 96JP-0352580.

XX PR 04-MAR-1996; 96JP-0073217.

XX (SUNR) SUNTORY LTD.

XX PI Magota K, Masuda T, Suzuki Y, Yabuta M;

XX WPI; 1997-437479/41.

XX Secreted forms of Kex2 protease - useful for cleaving chimeric proteins

PS Disclosure; page 25; 82pp; English.

XX This is the human parathyroid hormone peptide hPTH (residues 1-84). This is used in the construction of a chimeric protein betaGal-139S(FM)PPH84. The enzyme Kex2 protease can be used for excision of a desired protein from a chimeric protein comprising the desired protein and an Arg-Arg, Lys-Arg or Pro-Arg sequence adjacent to the N terminus of the desired protein. It can be specifically used for cleaving this human parathyroid hormone peptide hPTH(1-84) or peptide hPTH(1-34) from chimeric proteins such as the beta Gal-139S(FM)PPH84 or CATPH34. Derivatives of Kex2 protease, and especially kex2-660 can also cleave such chimeric proteins with high specificity and efficiency even in the absence of urea.

XX Sequence 84 AA;

Query Match 98.8%; Score 417; DB 18; Length 84;

Best Local Similarity 98.8%; Pred. No. 2.2e-41;

Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE 60

DB 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE 61

QY 61 SHEKSLGEANKADYNVLTAKSQ 83

DB 62 SHEKSLGEADKADYNVLTAKSQ 84

RESULT 12

AAW2577

ID AAY02577 standard; protein; 84 AA.

XX AC AAY02577;

XX 16-JUL-1999 (first entry)

DE Human parathyroid hormone (hPTH) protein.

KW Human parathyroid hormone; hPTH; bone mass;
KW 3-(substituted phenoxy)benzo(b)thiophene compound;
KW bone loss treatment; osteoporosis.

XX OS Homo sapiens.

XX PN WO9918945-A1.

XX PD 22-APR-1999.

XX PF 05-OCT-1998; 98WO-US20848.

XX PR 14-OCT-1997; 97US-0061800.

XX PA (ELIL) LILLY & CO ELI.

XX PI Sato M;

XX WPI; 1999-287871/24.

XX Method of building bone mass by co-administration of a parathyroid hormone with a 3-(substituted phenoxy)benzo(b)thiophene compound

XX Claim 5; Page 38; 48pp; English.

XX The present sequence represents human parathyroid hormone (hPTH). It, and its fragments, are used in the method of the invention. The specification describes a method for building bone mass, comprising administration of a parathyroid hormone with a 3-(substituted phenoxy)benzo(b)thiophene compound. The method is used for treatment of bone loss, e.g. in osteoporosis.

XX Sequence 84 AA;

Query Match 98.8%; Score 417; DB 20; Length 84;

Best Local Similarity 98.8%; Pred. No. 2.2e-41;

Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE 60

DB 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE 61

QY 61 SHEKSLGEANKADYNVLTAKSQ 83

DB 62 SHEKSLGEADKADYNVLTAKSQ 84

RESULT 13

AAW2577

ID AAB91082 standard; Peptide; 84 AA.

XX AC AAB91082;

XX 22-JUN-2001 (first entry)

DE Parathyroid hormone (PTH) related peptide SEQ ID NO:256.

KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidy; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX OS Homo sapiens.

XX Synthetic.

XX WO200069900-A2.
 XX 23-NOV-2000.
 XX 17-MAY-2000; 2000WO-US13576.
 XX 17-MAY-1999; 99US-0134406.
 PR 10-SEP-1999; 99US-0153406.
 PR 15-OCT-1999; 99US-0159783.
 XX (CONJ-) CONJUCHEM INC.
 XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
 XX WPI; 2001-112059/12.
 XX Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity
 PT
 XX Disclosure; Page 274-275; 733pp; English.
 PS
 CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention.
 XX
 XX Sequence 84 AA;
 SQ
 Query Match 98.8%; Score 417; DB 22; Length 84;
 Best Local Similarity 98.8%; Pred. No. 2.2e-41;
 Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 1 VSEIQLMHNILGKHLNSMERVEWLKKLQDVHNFVALGAPLAPRDAGSORPKKEDNVLVE 60
 DB 2 VSEIQLMHNILGKHLNSMERVEWLKKLQDVHNFVALGAPLAPRDAGSORPKKEDNVLVE 61
 OY 61 SHEKSLGEANKADVNLTKAKSQ 83
 DB 62 SHEKSLGEANKADVNLTKAKSQ 84
 RESULT 14
 ABG71472
 ID ABG71472 standard; Protein; 84 AA.
 XX AC ABG71472;
 XX 28-FEB-2003 (first entry)
 DT Human parathyroxin (hPTH) related protein.
 XX Parathyroxin; hPTH.
 XX Unidentified.
 OS
 XX CN1953115-A.
 PN 12-JUN-2002.

XX 13-NOV-2000; 2000CN-0133573.
 XX 13-NOV-2000; 2000CN-0133573.
 XX (MEIB/) MEI B.
 XX Huang X, You Z, Li S;
 XX WPI; 2002-751425/82.
 DR N-PSDB; ABS57477.
 XX
 PT Synthesis and expression of recombinant human parathyroxin gene -
 XX Disclosure; Fig 1; 16pp; Chinese.
 PS
 XX The invention relates to a DNA sequence containing a fragment of the
 CC human parathyroxin (hPTH) gene. The invention also relates to splicing
 CC artificially synthesised oligodeoxynucleotide chains by PCR and preparing
 CC fusion or non-fusion expressed engineering bacteria of recombination
 CC protein hPTH through integrating the gene in different expression
 CC carriers. This sequence represents a human parathyroxin related protein.
 XX
 SQ Sequence 84 AA;
 Query Match 98.8%; Score 417; DB 23; Length 84;
 Best Local Similarity 98.8%; Pred. No. 2.2e-41;
 Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 1 VSEIQLMHNILGKHLNSMERVEWLKKLQDVHNFVALGAPLAPRDAGSORPKKEDNVLVE 60
 DB 2 VSEIQLMHNILGKHLNSMERVEWLKKLQDVHNFVALGAPLAPRDAGSORPKKEDNVLVE 61
 OY 61 SHEKSLGEANKADVNLTKAKSQ 83
 DB 62 SHEKSLGEANKADVNLTKAKSQ 84
 RESULT 15
 AAE23726
 ID AAE23726 standard; peptide; 84 AA.
 XX AC AAE23726;
 XX 10-SEP-2002 (first entry)
 DT Human parathyroid hormone (hPTH) peptide (1-84).
 DE Human parathyroid hormone; hPTH; PTH-related peptide; PTHrP; eczema;
 KW hyperproliferative skin disorder; psoriasis; ichthyosis; skin cancer;
 KW acne; actinic keratosis; alopecia; gene therapy.
 XX Homo sapiens.
 OS
 XX WO200228420-A2.
 PN 11-APR-2002.
 XX 05-OCT-2001; 2001WO-US31082.
 XX 06-OCT-2000; 2000US-238134P.
 PR (HOLI/) HOLICK M F.
 XX Holick MF;
 PI WPI; 2002-452304/48.
 DR N-PSDB; AAD37995.
 XX
 PT Regulating mammalian skin or hair cell proliferation and
 PT differentiation by administering nucleic acids encoding peptides
 PT derived from N-terminal region of human parathyroid hormone (hPTH) or
 PT hPTH-related protein.

XX
PS
XX
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
XX
SQ

Claim 5; Fig 18; 56pp; English.

The invention relates to a method for regulating proliferation or enhancing differentiation of mammalian skin or hair cell. The method involves administering nucleic acids encoding peptides derived from N-terminal region of human parathyroid hormone (hPTH) or hPTH-related peptide (PTHrP). The method is used for inhibiting hyperproliferative skin disorders such as psoriasis, ichthyosis, eczema, acne, actinic keratosis, skin cancer, for inhibiting hair growth or preventing hair regrowth. It is useful for stimulating cell growth, rejuvenating aged skin, preventing skin wrinkles, treating skin wrinkles, enhancing wound healing, stimulating hair growth, maintaining hair growth, treating or preventing female or male pattern baldness, for treating chemotherapy induced alopecia and also for stimulating epidermal cell growth or hair follicle cell growth. The method is also used in gene therapy. The present sequence is hPTH peptide.

Sequence 84 AA:

Query Match 98.8%; Score 417; DB 23; Length 84;
Best Local Similarity 98.8%; Pred. No. 2.2e-41;
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 VSETLMHNLGKHLNSMERVWLKKLQDVHNFVALGAPLAPRDAGSQRPKKEDNVLVE 60
DB 2 VSETLMHNLGKHLNSMERVWLKKLQDVHNFVALGAPLAPRDAGSQRPKKEDNVLVE 61
QY 61 SHEKSLGEANKADVNLTKAKSQ 83
DB 62 SHEKSLGEANKADVNLTKAKSQ 84

Search completed: October 9, 2003, 08:10:45
Job time : 59.9627 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October -9, 2003, 08:08:56 ; Search time 16.1045 Seconds
(without alignments)
242.368 Million cell updates/sec

Title: US-09-928-048a-4
Perfect score: 422
Sequence: 1 VSEIQLMHNGLKHLNSMERY.....KSLGEANKADVNVLTAKSQ 83

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	417	98.8	115	1 PTHY_HUMAN	P01270
2	410	97.2	115	1 PTHY_MACFA	P02135
3	366	86.7	115	1 PTHY_CANFA	P52112
4	359	85.1	115	1 PTHY_BOVIN	P01268
5	355	84.1	115	1 PTHY_PIG	P01269
6	311	73.7	115	1 PTHY_RAT	P04089
7	174.5	41.4	119	1 PTHY_CHICK	P01573
8	72.5	17.2	824	1 SVL_THEME	Q9WY15
9	72	17.1	1257	1 RBBI_HUMAN	P23174
10	69.5	16.5	555	1 UL25_HSV62	P52537
11	68	16.1	606	1 GLMS_FUSNN	P52537
12	67	15.9	443	1 HSLU_VIBCH	Q8F965
13	66.5	15.8	378	1 UL25_HSV66	Q9KNG7
14	66.5	15.8	555	1 UL25_HSV60	Q9KNG7
15	66	15.6	396	1 DPO4_CLOAB	P52387
16	65	15.4	1244	1 MX1_CAEEL	P52387
17	64.5	15.3	205	1 KGA_CHLPN	Q09591
18	64.5	15.3	668	1 SGL_PIG	Q92961
19	64	15.2	642	1 FLTD_CAMJE	Q92961
20	63.5	15.0	1270	1 ITN1_XENLA	Q92961
21	63	14.9	992	1 FLT3_MOUSE	Q92961
22	63	14.9	1033	1 Y328_MYCPN	Q92961
23	63	14.9	1388	1 ROD_TOBAC	Q92961
24	63	14.9	1937	1 MYH8_HUMAN	Q92961
25	62.5	14.8	370	1 YAA4_HELPY	Q92961
26	62.5	14.8	632	1 DNK1_ACTAC	Q92961
27	62.5	14.8	1658	1 ITN2_MOUSE	Q92961
28	62	14.7	300	1 YSDO_ECOLI	Q92961
29	62	14.7	1041	1 DD16_HUMAN	Q92961
30	61.5	14.6	366	1 YE05_HAEIN	Q92961
31	61	14.5	429	1 DPD2_ORYSA	Q92961
32	61	14.5	910	1 HUL5_YEAST	Q92961
33	60.5	14.3	942	1 PKL1_HUMAN	Q92961

34	60.5	14.3	1721	1 ITN1_HUMAN	Q15811
35	60	14.2	455	1 HYIN_PSESS	Q15811
36	60	14.2	668	1 DCRA_DESVH	P06618
37	60	14.2	1027	1 KINN_MOUSE	P35841
38	60	14.2	1032	1 KINN_MOUSE	P33175
39	60	14.2	1084	1 MYSS_RABIT	Q12840
40	60	14.2	1172	1 SYK2_MCTU	P02562
41	60	14.2	1935	1 MYSS_CYPCT	P94974
42	60	14.2	1938	1 MYH4_RABIT	Q08339
43	60	14.2	1940	1 MYH3_CHICK	Q28641
44	60	14.2	2390	1 SPCP_HUMAN	P02565
45	59.5	14.1	437	1 MURC_STAAU	Q15020
					Q31211

ALIGNMENTS

RESULT 1	
PTHY_HUMAN	
ID	PTHY_HUMAN
AC	P01270;
DT	21-JUL-1986 (Rel. 01, Created)
DT	13-AUG-1987 (Rel. 05, Last sequence update)
DT	15-SEP-2003 (Rel. 42, Last annotation update)
DE	Parathyroid hormone precursor (Parathyrin) (PTH) (Parathormone).
GN	PTH.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=82150870; PubMed=6950381;
RA	Hendy G.N., Kronenberg H.M., Potts J.T. Jr., Rich A.;
RT	"Nucleotide sequence of cloned cDNAs encoding human preproparathyroid hormone."
RT	Proc. Natl. Acad. Sci. U.S.A. 80:2127-2131(1983).
RN	[3]
RP	SEQUENCE OF 26-37.
RX	MEDLINE=74174967; PubMed=4833516;
RA	Jacobs J.W., Kemper B., Niall H.D., Habener J.F., Potts J.T. Jr.;
RT	"Structural analysis of human parathyroid hormone by a new microsequencing approach."
RT	Nature 249:155-157(1974).
RN	[4]
RP	SEQUENCE OF 32-68.
RX	MEDLINE=74111656; PubMed=4521809;
RA	Niall H.D., Sauer R.T., Jacobs J.W., Keutmann H.T., Segre G.V.,
RA	O'Riordan J.L.H., Aurbach G.D., Potts J.T. Jr.;
RT	"The amino-acid sequence of the amino-terminal 37 residues of human parathyroid hormone."
RT	Proc. Natl. Acad. Sci. U.S.A. 71:384-388(1974).
RN	[5]
RP	SEQUENCE OF 61-83 AND 84-115.
RX	MEDLINE=79082855; PubMed=728431;
RA	Keutmann H.T., Sauer M.M., Hendy G.N., O'Riordan J.L.H.,
RA	Potts J.T. Jr.;
RT	"Complete amino acid sequence of human parathyroid hormone."
RT	Biochemistry 17:5723-5729(1978).
RN	[6]
RP	SEQUENCE OF 75-100.
RA	Keutmann H.T., Niall H.D., Jacobs J.W., Barling P.M., Hendy G.N.,
RA	O'Riordan J.L.H., Potts J.T. Jr.;
RL	(In) Talmadge R.V., Owen M., Parsons J.A. (eds.);
RL	Calcium-regulating hormones, pp.9-14, Excerpta Medica Foundation,
RL	Amsterdam (1975).

[7] REVISIONS.
 RP MEDLINE=75146516; PubMed=1125201;
 RA Keutmann H.T., Niall H.D., O'Riordan J.L.H., Potts J.T. Jr.;
 RT "A reinvestigation of the amino-terminal sequence of human
 parathyroid hormone."
 RL Biochemistry 14:1842-1847(1975).
 [8]
 RP SYNTHESIS OF 32-65.
 RA Tregear G.W., van Rietschoten J., Green E., Niall H.D.,
 RA Keutmann H.T., Parsons J.A., O'Riordan J.L.H., Potts J.T. Jr.;
 RT "Solid-phase synthesis of the biologically active N-terminal 1-34
 peptide of human parathyroid hormone."
 RL Hoppe-Seyler's Z. Physiol. Chem. 355:415-421(1974).
 [9]
 RP SYNTHESIS OF 32-65.
 RA Andreatta R.H., Hartmann A., Joehl A., Kamber B., Maier R.,
 RA Rinkler B., Rittel W., Sieber P.;
 RT "Synthesis of sequence 1-34 of human parathyroid hormone."
 RL Helv. Chim. Acta 56:470-473(1973).
 [10]
 RP STRUCTURE BY NMR OF 32-65.
 RA MEDLINE=9129748; PubMed=2069952;
 RA Klaus W., Dieckmann T., Wray V., Schomburg D., Wingender E., Mayer H.;
 RT "Investigation of the solution structure of the human parathyroid
 hormone fragment (1-34) by 1H NMR spectroscopy, distance geometry,
 and molecular dynamics calculations."
 RL Biochemistry 30:6936-6942(1991).
 [11]
 RP STRUCTURE BY NMR OF 32-65.
 RA MEDLINE=93345518; PubMed=8344299;
 RA Barden J.A., Cuthbertson R.M.;
 RT "Stabilized NMR structure of human parathyroid hormone(1-34).";
 RL Eur. J. Biochem. 215:315-321(1993).
 [12]
 RP STRUCTURE BY NMR OF 32-68.
 RA MEDLINE=95318084; PubMed=7797503;
 RA Marx U.C., Adermann K., Bayer P., Adermann K., Eychart A.,
 RA Sticht H., Walter S., Schmid F.-X., Jaenicke R., Forssmann W.-G.,
 RA Roesch P.;
 RT "Structure of human parathyroid hormone 1-37 in solution."
 RL J. Biol. Chem. 270:15194-15202(1995).
 [13]
 RP STRUCTURE BY NMR OF 32-70.
 RA MEDLINE=20090619; PubMed=10623601;
 RA Marx U.C., Adermann K., Bayer P., Forssmann W.-G., Rosch P.;
 RT "Solution structures of human parathyroid hormone fragments
 hPTH(1-34) and hPTH(1-39) and bovine parathyroid hormone fragment
 bPTH(1-37).";
 RL Biochem. Biophys. Res. Commun. 267:213-220(2000).
 [14]
 RP VARIANT ARG-18.
 RA MEDLINE=91009811; PubMed=2212001;
 RA Arnold A., Horst S.A., Gardella T.J., Baba H., Levine M.A.,
 RA Kronenberg H.M.;
 RT "Mutation of the signal peptide-encoding region of the
 preproparathyroid hormone gene in familial isolated
 hypoparathyroidism."
 RL J. Clin. Invest. 86:1084-1087(1990).
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 CC BONE AND PREVENTING THEIR RENAL EXCRETION.
 CC -1- DISEASE: Defects in PTH are a cause of familial isolated
 CC hypoparathyroidism (FIH) [MIM:146200].
 CC -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>)

or send an email to license@isb-sib.ch.
 CC
 CC EMBL: J00301; AAA60215.1; --
 DR EMBL: V00597; CAA23843.1; --
 DR EMBL: A29146; CAA01956.1; --
 DR PIR: A19339; PTHU.
 DR PDB: 1HPH; 10-JUL-95.
 DR PDB: 1HTH; 15-OCT-97.
 DR PDB: 1ZNA; 12-MAR-97.
 DR PDB: 1ZNB; 12-MAR-97.
 DR PDB: 1ZWD; 12-MAR-97.
 DR PDB: 1ZWE; 12-MAR-97.
 DR PDB: 1ZWF; 16-JUN-97.
 DR PDB: 1ZWC; 16-JUN-97.
 DR PDB: 1BWX; 14-JAN-00.
 DR PDB: 1HPY; 14-JAN-00.
 DR PDB: 1ETI; 06-SEP-00.
 DR PDB: 1ETZ; 06-SEP-00.
 DR PDB: 1FVY; 31-DEC-02.
 DR GeneW: HGNC:9606; PTH.
 DR MIM: 168450; --
 DR MIM: 146200; --
 DR GO: GO:0008492; F:AMP generating peptide activity; TAS.
 DR GO: GO:0005180; F:peptide hormone; TAS.
 DR GO: GO:0007367; P:cell-cell signaling; TAS.
 DR GO: GO:0007186; P:G-protein coupled receptor protein signalin...; TAS.
 DR GO: GO:0008628; P:induction of apoptosis by hormones; TAS.
 DR GO: GO:0001501; P:skeletal development; TAS.
 DR InterPro: IPR001415; Parathyrd_hrm.
 DR InterPro: IPR003625; Pthyrdorm_sub.
 DR Pfam: PF01279; Parathyroid; 1.
 DR ProDom: PD010687; Pthyrdorm_sub; 1.
 DR SMART: SM00087; PTH; 1.
 DR PROSITE: PS00335; PARATHYROID; 1.
 DR Hormone; Signal; Disease mutation; 3D-structure.
 FT SIGNAL 1 25
 FT PROPEP 26 31
 FT CHAIN 32 115
 FT VARIANT 18 18
 FT
 FT CONFLICT 107 107
 FT HELIX 36 41
 FT TURN 42 43
 FT HELIX 49 63
 FT TURN 64 66
 FT SEQUENCE 115 AA; 12861 MW; 849015736AE5597 CRC64;
 SQ
 Query Match 98.8%; Score 417; DB 1; Length 115;
 Best Local Similarity 98.8%; Pred. No. 9.4e-39;
 Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VSEIQLMHNGLKHLNSMERVWLKKLDVHNFVALGAPLAPRDSQRRPKEDNVLYE 60
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 33 VSEIQLMHNGLKHLNSMERVWLKKLDVHNFVALGAPLAPRDSQRRPKEDNVLYE 92
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 61 SHEKSLGEANKADVNVLTKAKSQ 83
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 93 SHEKSLGEANKADVNVLTKAKSQ 115
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 RESULT 2
 PTH_MACFA STANDARD; PRT: 115 AA.
 ID PTH_MACFA
 AC Q9XTJ35;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Parathyroid hormone precursor (Parathyria) (PTH).
 GN PTH
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

CC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Malaivijitnond S., Takenaka O.;
 RT "Nucleotide sequences of parathyroid gene in five species of macaque
 of Thailand.";
 RL J. Sci. Res. Chulalongkorn Univ. 23:135-142(1998).
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 BONE AND PREVENTING THEIR RENAL EXCRETION.
 CC -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AF130257; AAD42777.1;
 DR HSSP: P01270; 1HPY.
 DR InterPro: IPR001415; Parathyroid_hrm.
 DR Pfam: PF01279; Parathyroid; 1.
 DR ProDom: PD010687; Pthyrhorm_sub; 1.
 DR SMART: SM00087; PTH; 1.
 DR PROSITE: PS00335; PARATHYROID; 1.
 KW Hormone; Signal.
 FT SIGNAL 1 25 BY SIMILARITY.
 FT PROPEP 26 31 BY SIMILARITY.
 FT CHAIN 32 115 PARATHYROID HORMONE.
 SQ SEQUENCE 115 AA; 12890 MW; 8C2500EF24BE597 CRC64;
 Query Match 97.2%; Score 410; DB 1; Length 115;
 Best Local Similarity 95.2%; Pred. No. 5.5e-38;
 Matches 79; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VSEIQLMHNGLKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPKKEDNVLYE 60
 DB 33 VSEIQLMHNGLKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPKKEDNVLYE 92
 QY 61 SHEKSLGEANKADVNVLTKAKSQ 83
 DB 93 SHEKSLGEANKADVDVLTAKSQ 115
 Query Match 97.2%; Score 410; DB 1; Length 115;
 Best Local Similarity 95.2%; Pred. No. 5.5e-38;
 Matches 79; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VSEIQLMHNGLKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPKKEDNVLYE 60
 DB 33 VSEIQLMHNGLKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPKKEDNVLYE 92
 QY 61 SHEKSLGEANKADVNVLTKAKSQ 83
 DB 93 SHEKSLGEANKADVDVLTAKSQ 115
 RESULT 3
 ID PTHY_CANFA STANDARD; PRT; 115 AA.
 AC P52212;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Parathyroid hormone precursor (Parathyrin) (PTH).
 GN PTH.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Parathyroid;
 RX MEDLINE=95369696; PubMed=7642102;
 RA Rosol T.J., Steimeyer C.L., McCauley L.K., Greene A.,
 RA DeWille J.W., Capen C.C.;
 RT "Sequences of the cDNAs encoding canine parathyroid hormone-related
 protein and parathyroid hormone."
 RL Gene 160:241-243(1995).
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 BONE AND PREVENTING THEIR RENAL EXCRETION.
 CC -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
 CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U15662; AAA82584.1;
 DR FIR: JC4202; JC4202.
 DR HSSP: P01268; 12WC.
 DR InterPro: IPR001415; Parathyroid_hrm.
 DR Pfam: PF01279; Parathyroid; 1.
 DR ProDom: PD010687; Pthyrhorm_sub; 1.
 DR SMART: SM00087; PTH; 1.
 DR PROSITE: PS00335; PARATHYROID; 1.
 KW Hormone; Signal.
 FT SIGNAL 1 25 BY SIMILARITY.
 FT PROPEP 26 31 BY SIMILARITY.
 FT CHAIN 32 115 PARATHYROID HORMONE.
 SQ SEQUENCE 115 AA; 12957 MW; FC38F77F1C8CFE56 CRC64;
 Query Match 86.7%; Score 366; DB 1; Length 115;
 Best Local Similarity 86.7%; Pred. No. 3.5e-33;
 Matches 72; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
 QY 1 VSEIQLMHNGLKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPKKEDNVLYE 60
 DB 33 VSEIQLMHNGLKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSQRPKKEDNVLYE 92
 QY 61 SHEKSLGEANKADVNVLTKAKSQ 83
 DB 93 SYOKSLGEADKADVDVLTAKSQ 115
 RESULT 4
 ID PTHY_BOVIN STANDARD; PRT; 115 AA.
 AC P01268;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Parathyroid hormone precursor (Parathyrin) (PTH).
 GN PTH.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=80056617; PubMed=388425;
 RA Kronenberg H.M., McDevitt B.E., Majzoub J.A., Nathans J., Sharp P.A.,
 RA Potts J.T. Jr., Rich A.;
 RT "Cloning and nucleotide sequence of DNA coding for bovine
 preproparathyroid hormone."
 RL Proc. Natl. Acad. Sci. U.S.A. 76:4981-4985(1979).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=82037785; PubMed=6170060;
 RA Weaver C.A., Gordon D.F., Kemper B.;
 RT "Introduction by molecular cloning of artifactual inverted sequences
 at the 5' terminus of the sense strand of bovine parathyroid hormone
 cDNA."
 RL Mol. Cell. Endocrinol. 28:411-424(1982).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83105964; PubMed=6185374;
 RA Weaver C.A., Gordon D.F., Kemper B.;
 RT "Nucleotide sequence of bovine parathyroid hormone messenger RNA."
 RL Mol. Cell. Endocrinol. 28:411-424(1982).
 RN [4]

RP SEQUENCE FROM N.A.
 RX MEDLINE-84262483; PubMed-6086460;
 RA Weaver C.A., Gordon D.F., Kissil M.S., Mead D.A., Kemper B.;
 RT "Isolation and complete nucleotide sequence of the gene for bovine
 RL parathyroid hormone."; Gene 28:319-329(1984).
 RN [5]
 RP SEQUENCE OF 26-115.
 RX MEDLINE-74142666; PubMed-4522780;
 RA Hamilton J.W., Niall H.D., Jacobs J.W., Keutmann H.T., Potts J.T. Jr.,
 RA Cohn D.V.;
 RT "The N-terminal amino-acid sequence of bovine parathyroid
 RL hormone."; Proc. Natl. Acad. Sci. U.S.A. 71:653-656(1974).
 RN [6]
 RP SEQUENCE OF 32-115.
 RX MEDLINE-71076162; PubMed-5531031;
 RA Niall H.D., Keutmann H.T., Sauer R., Hogan M.L., Dawson B.F.,
 RA Aurbach G.D., Potts J.T. Jr.;
 RT "The amino acid sequence of bovine parathyroid hormone I.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 351:1586-1588(1970).
 RN [7]
 RP SEQUENCE OF 32-115.
 RX MEDLINE-71063634; PubMed-5275384;
 RA Brewer H.B. Jr., Ronan R.;
 RT "Bovine parathyroid hormone: amino acid sequence."; Proc. Natl. Acad. Sci. U.S.A. 67:1862-1869(1970).
 RN [8]
 RP SYNTHESIS OF 32-65.
 RX MEDLINE-71091588; PubMed-4322265;
 RA Potts J.T. Jr., Tregear G.W., Keutmann H.T., Niall H.D., Sauer R.,
 RA Defotis L.J., Dawson B.F., Hogan M.L., Aurbach G.D.;
 RT "Synthesis of a biologically active N-terminal tetra-tyrosine peptide
 RL of parathyroid hormone."; Proc. Natl. Acad. Sci. U.S.A. 68:63-67(1971).
 RN [9]
 RP STRUCTURE BY NMR OF 32-68.
 RX MEDLINE-20090619; PubMed-10623601;
 RA Marx U.C., Ademann K., Bayer F., Forssmann W.-G., Rosch P.;
 RT "Solution structures of human parathyroid hormone fragments
 RL hPTH(1-34) and hPTH(1-39) and bovine parathyroid hormone fragment
 RL bPTH(1-37)."; Biochem. Biophys. Res. Commun. 267:213-220(2000).
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 CC BONE AND PREVENTING THEIR RENAL EXCRETION.
 CC -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; V00106; CAA23439.1; -
 DR EMBL; J00024; AAA30747.1; -
 DR EMBL; K01938; AAA30749.1; -
 DR EMBL; M25082; AAA30748.1; -
 DR FIR; A24949; PTBO.
 DR PDB; 1ZWC; 12-MAR-97.
 DR InterPro: IPR001415; Parathyroid_hrm.
 DR InterPro: IPR003625; Pthyrhorm_sub.
 DR Pfam; PF01279; Parathyroid; 1.
 DR ProDom; PD010687; Pthyrhorm_sub; 1.
 DR SMART; SM00087; PTH; 1.
 DR PROSITE; PS00335; PARATHYROID; 1.
 KW Hormone; Signal; 3D-structure.
 FT SIGNAL 1 25
 FT PROPEP 26 31
 FT CHAIN 32 115 PARATHYROID HORMONE.
 FT CONFLICT 106 106 V -> G (IN REF. 4).
 FT HELIX 37 40

FT TURN 41 42
 FT TURN 51 52
 FT HELIX 53 60
 FT TURN 61 63
 SQ SEQUENCE 115 AA; 12980 MW; 2ED246B348880710 CRC64;
 Query Match 85.1%; Score 359; DB 1; Length 115;
 Best Local Similarity 85.5%; Pred. No. 2e-32;
 Matches 71; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
 QY 1 VSEIQLMNHLGKHLNLMERVELRKQLQDVHNFVALGAPLAPRDAGSQPRPKKEDNVLYE 60
 DB 33 VSEIQFMNHLGKHLNLMERVELRKQLQDVHNFVALGASIAIYRDGSSQPRPKKEDNVLYE 92
 QY 61 SHEKSLGEAKADVNVLTKAKSQ 83
 DB 93 SHOKSLGEAKADVDVLTKAKPQ 115
 RESULT 5
 PTHY_PIG STANDARD; PRT; 115 AA.
 ID PTHY_PIG
 AC P01269;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Parathyroid hormone precursor (Parathyrin) (PTH).
 GN PTH.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-87316938; PubMed-3628009;
 RA Schmelzer H.-J., Gross G., Widera G., Mayer H.;
 RT "Nucleotide sequence of a full-length cDNA clone encoding
 RL preproparathyroid hormone from pig and rat."; Nucleic Acids Res. 15:6740-6740(1987).
 RN [2]
 RP SEQUENCE OF 26-115.
 RX MEDLINE-76018954; PubMed-1164500;
 RA Chu L.H., Huang W.-Y., Littledike E.T., Hamilton J.W., Cohn D.V.;
 RT "Porcine parathyroid hormone. Identification, biosynthesis, and
 RL partial amino acid sequence."; Biochemistry 14:3631-3635(1975).
 RN [3]
 RP SEQUENCE OF 32-115.
 RX MEDLINE-74253317; PubMed-4840833;
 RA Sauer R.T., Niall H.D., Hogan M.L., Keutmann H.T., O'Riordan J.L.H.,
 RA Potts J.T. Jr.;
 RT "The amino acid sequence of porcine parathyroid hormone."; Biochemistry 13:1994-1999(1974).
 RL Biochemistry 13:1994-1999(1974).
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 CC BONE AND PREVENTING THEIR RENAL EXCRETION.
 CC -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X05722; CAA29193.1; -
 DR PIR; B26806; PTPG.
 DR HSSP; P01270; 1BW.
 DR InterPro: IPR001415; Parathyroid_hrm.
 DR InterPro: IPR003625; Pthyrhorm_sub.
 DR Pfam; PF01279; Parathyroid; 1.
 DR ProDom; PD010687; Pthyrhorm_sub; 1.
 DR SMART; SM00087; PTH; 1.

```

DR PROSITE; PS00335; PARATHYROID; 1.
KW Hormone; Signal.
FT SIGNAL 1 25
FT PROPEP 26 31
FT CHAIN 32 115
SQ SEQUENCE 115 AA; 12852 MW; 9FEBBCDE614BAC16 CRC64;

Query Match
Best Local Similarity 84.1%; Score 355; DB 1; Length 115;
Matches 70; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 VSEIQLMHLNGLKHLNLSMERVENLRKKLQDVHNFVALGAPLAPRDAGSORPKKEDNVLYE 60
DB 33 VSEIQLMHLNGLKHLNLSMERVENLRKKLQDVHNFVALGASIVHRDGGSORPKKEDNVLYE 92
QY 61 SHEKSLGEANKADVNVLTKAKSQ 83
DB 93 SHQKSLGEADKAADVNLIRAKPQ 115

RESULT 6
PTHY_RAT
ID PTHY_RAT STANDARD; PRT; 115 AA.
AC P04089; Q63473;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
GN PTH.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP MEDLINE=84135846; PubMed=6321505;
RA Heinrich G., Kronenberg H.M., Potts J.T. Jr., Habener J.F.;
RT "Gene encoding parathyroid hormone. Nucleotide sequence of the rat
RT gene and deduced amino acid sequence of rat preproparathyroid
RT hormone."
RL J. Biol. Chem. 259:3320-3329(1984).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=84135846; PubMed=6321505;
RA Schmelzer H.-J., Gross G., Widera G., Mayer H.;
RT "Nucleotide sequence of a full-length cDNA clone encoding
RT preproparathyroid hormone from pig and rat."
RL Nucleic Acids Res. 15:6740-6740(1987).
RN [3]
RP SEQUENCE OF 10-115 FROM N.A.
RC TISSUE=Parathyroid;
RA Schmelzer H.-J., Gross G., Mayer H.;
RT "Nucleotide sequence of cloned cDNA encoding rat prepro parathyroid
RT hormone."
RL Adv. Gene Technol. 21:228-229(1984).
RN [4]
RP SEQUENCE OF 32-115 FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain, Liver, and Parathyroid;
RX MEDLINE=96079910; PubMed=7588314;
RA Nutley M.T., Parimi S.A., Harvey S.;
RT "Sequence analysis of hypothalamic parathyroid hormone messenger
RT ribonucleic acid."
RL Endocrinology 136:5600-5607(1995).
RN [5]
RP FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
CC -!- TISSUE SPECIFICITY: HYPOTHALAMUS AND PARATHYROID GLAND.
CC -!- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial

```

```

CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; K01268; AAA41979.1;
DR EMBL; X05721; AAA29192.1;
DR EMBL; M54875; AAA57156.1;
DR EMBL; S80127; NOT_ANNOTATED_CDS.
DR PIR; A05091; A05091.
DR KSSP; P01270; 12WB.
DR InterPro; IPR001415; Parathyrd_hrm.
DR InterPro; IPR003625; Pthyhorm_sub.
DR Pfam; PF01279; Parathyroid; 1.
DR ProDom; PD010687; Pthyhorm_sub; 1.
DR SMART; SM00087; PTH; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
KW Hormone; Signal.
FT SIGNAL 1 25
FT PROPEP 26 31
FT CHAIN 32 115
FT CONFLICT 18 18
FT CONFLICT 23 23
FT CONFLICT 33 33
FT CONFLICT 62 62
SQ SEQUENCE 115 AA; 12722 MW; 7B434CFCAS28B230 CRC64;

Query Match
Best Local Similarity 73.7%; Score 311; DB 1; Length 115;
Matches 60; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 VSEIQLMHLNGLKHLNLSMERVENLRKKLQDVHNFVALGAPLAPRDAGSORPKKEDNVLYE 60
DB 33 VSEIQLMHLNGLKHLNLSMERVENLRKKLQDVHNFVALGASIVHRDGGSORPKKEDNVLYE 92
QY 61 SHEKSLGEANKADVNVLTKAKSQ 83
DB 93 GNSKSLGEGKADVDVLYKAKSQ 115

RESULT 7
PTHY_CHICK
ID PTHY_CHICK STANDARD; PRT; 119 AA.
AC P15743;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DE 15-JUL-1998 (Rel. 36, Last annotation update)
DE Parathyroid hormone precursor (PTH).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89219100; PubMed=2710135;
RA Russell J., Sherwood L.M.;
RT "Nucleotide sequence of the DNA complementary to avian (chicken)
RT preproparathyroid hormone mRNA and the deduced sequence of the
RT hormone precursor."
RL Mol. Endocrinol. 3:325-331(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89284968; PubMed=3251402;
RA Khosla S., Denay M., Pines M., Hurwitz S., Potts J.T. Jr.,
RA Kronenberg H.M.;
RT "Nucleotide sequence of cloned cDNAs encoding chicken
RT preproparathyroid hormone."
RL J. Bone Miner. Res. 3:689-698(1988).
CC -!- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
CC -!- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

```

CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL: M31604; AAA49093.1; -
 DR EMBL: M36522; AAB02866.1; -
 DR FIRM: A34937; A34937.
 DR HSP: P01270; LHPY.
 DR InterPro: IPR001415; Parathyroid_hrm.
 DR InterPro: IPR003625; Pthyrohm_sub.
 DR Pfam: PF01279; Parathyroid; 1.
 DR ProDom: PD010687; Pthyrohm_sub; 1.
 DR SMART: SM00087; PTH; 1.
 DR PROSITE: PS00335; PARATHYROID; 1.
 DR Hormone; Signal.
 KW SIGNAL 1 25
 FT PROPEP 26 31
 FT CHAIN 32 119 PARATHYROID HORMONE.
 FT CHAIN 119 AA; 13943 MW; B309D8E772997F6E CRC64;
 SQ SEQUENCE

Query Match 41.4%; Score 174.5; DB 1; Length 119;
 Best Local Similarity 44.7%; Pred. No. 3e-12;
 Matches 42; Conservative 14; Mismatches 17; Indels 21; Gaps 2;

QY 1 VSEIQLMNLGKHLNSMERVLRKKLDVHNFVALGAPLAPRDAGSQPRKKNVLVE 60
 DB 33 VSEQLMNLGKHLNSMERVLRKKLDVHNFVALGAPLAPRDAGSQPRKKNVLVE 84
 QY 61 -----SHEKSLGEANKADNVNLTAK 81
 DB 85 IRRRLPEHLRAVQKKSIDLDKAYMNVLTAK 118

RESULT 8
 ID SYL_THEMA STANDARD; PRT; 824 AA.
 AC Q9WV15;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine-tRNA ligase) (LeuRS).
 GN LEUS OR TM0168.
 OS Thermotoga maritima.
 OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
 OX NCBI_Taxid=2330;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MSB / DSM 3109;
 RX MEDLINE=99287316; PubMed=10360571;
 RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
 Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
 McDonald L., Utterback T.R., Malek J.A., Linher K.A., Garrett M.M.,
 Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
 Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
 Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
 RT "Evidence for lateral gene transfer between Archaea and Bacteria from
 RL genome sequence of Thermotoga maritima";
 RL Nature 399:323-329(1999).
 CC -1- CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP +
 CC diphosphate + L-leucyl-tRNA(Leu).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL: AE001702; AAD35261.1; -
 DR PIR: F72408; F72408.
 DR TIGR: TM0168; -
 DR HAMAP: MF_00049; -; 1.
 DR InterPro: IPR002302; Leu-trnasynthla.
 DR InterPro: IPR002300; tRNA-synt_la.
 DR InterPro: IPR001412; tRNA-synt_1.
 DR Pfam: PF00133; tRNA-synt_1; 1.
 DR PRINTS: PRO0985; TRNASYNTHLEU.
 DR TIGRFAMs: TIGR00396; leuS_bact; 1.
 DR PROSITE: PS00178; AA_TRNA_LIGASE_I; 1.
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 KW Complete proteome.
 FT SITE 41 51 "HIGH" REGION.
 FT SITE 580 584 "KMSKS" REGION.
 FT BINDING 583 583 ATP (BY SIMILARITY).
 FT BINDING 824 AA; 95624 MW; 7CB0252A76A844EC CRC64;
 SQ SEQUENCE

Query Match 17.2%; Score 72.5; DB 1; Length 824;
 Best Local Similarity 23.3%; Pred. No. 3.7;
 Matches 21; Conservative 25; Mismatches 25; Indels 19; Gaps 4;

QY 4 IOLMNLGKHLNSMERVLRKKLDVHNFVALGAPLAPRDAGSQPRKKNVLVE 55
 DB 692 MELVNLHSLQYLSNVQPEWNRKLLREIVEKLTALSPFAPHLAEFWHDLGN-----D 744
 QY 56 NVLVE-----SHEKSLGEANKADNVNLTAK 81
 DB 745 SLVVOGSWPSYDPKALEVEVEIAIQNGK 774

RESULT 9
 ID RBBL_HUMAN STANDARD; PRT; 1257 AA.
 AC P29374; Q15991; Q15992; Q15993;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Retinoblastoma-binding protein 1 (RBBP-1).
 GN RBBP1 OR RBP1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM I).
 RX MEDLINE=94020841; PubMed=8414517;
 RA Fattaey A.R., Helin K., Dembski M.S., Dyson N., Harlow E.,
 RA Vuocolo G.A., Hanobik M.G., Haskell K.M., Oliff A., Defeo-Jones D.,
 RA Jones R.E.;
 RT "Characterization of the retinoblastoma binding proteins RBP1 and
 RL RBP2";
 RL Oncogene 8:3149-3156(1993).
 RN [2]
 RP SEQUENCE FROM N.A., SUBCELLULAR LOCATION, AND ALTERNATIVE SPLICING.
 RX MEDLINE=93205410; PubMed=8455946;
 RA Otterson G.A., Kratzke R.A., Lin A.Y., Johnston P.G., Kaye F.J.;
 RT "Alternative splicing of the RBP1 gene clusters in an internal exon
 RL that encodes potential phosphorylation sites";
 RL Oncogene 8:949-957(1993).
 RN [3]
 RP SEQUENCE OF 855-1203 FROM N.A. (ISOFORM I).
 RX MEDLINE=91312450; PubMed=1857421;
 RA Defeo-Jones D., Huang P.S., Jones R.E., Haskell K.M., Vuocolo G.A.,
 RA Hanobik M.G., Huber H.E., Oliff A.;
 RT "Cloning of cDNAs for cellular proteins that bind to the
 RL retinoblastoma gene product";
 RL Nature 352:251-254(1991).
 CC -1- FUNCTION: INTERACTS WITH THE VIRAL PROTEIN-BINDING DOMAIN OF THE
 CC RETINOBLASTOMA PROTEIN.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms-3;

```
CC Name-I;
CC ISOId=P29374-1; Sequence=Displayed;
CC Name-II;
CC ISOId=P29374-2; Sequence=VSP_004373;
CC Name-III;
CC ISOId=P29374-3; Sequence=VSP_004371, VSP_004372;
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; S66427; AAB28543.1; -
DR EMBL; S57153; AAB25833.1; -
DR EMBL; S57160; AAB25834.1; -
DR EMBL; S57162; AAB25835.2; -
DR PIR; I58383; I58383;
DR Genew; HGNC:9885; RBBP1.
DR MIM; 180201;
DR GO; GO:0003634; C:nucleus; TAS.
DR GO; GO:0003515; F:protein binding activity; TAS.
DR GO; GO:0003700; F:transcription factor activity; TAS.
DR GO; GO:0003666; P:transcription from Pol II promoter; TAS.
DR InterPro; IPR001606; ARID.
DR InterPro; IPR000953; Chromo.
DR InterPro; IPR002999; Tudor.
DR Pfam; PF01398; ARID; 1.
DR SMART; SM00501; BRIGHT; 1.
DR SMART; SM00298; CHROMO; 1.
DR SMART; SM00333; TUDOR; 1.
KW Trans-acting factor; Nuclear protein; Alternative splicing.
FT DOMAIN 951 964
RETINOBLASTOMA PROTEIN BINDING
(POTENTIAL).
FT VARSPLIC 1106 1174
Missing (in isoform III).
FT VARSPLIC 1175 1175
N -> D (in isoform III).
FT VARSPLIC 1121 1174
Missing (in isoform II).
FT VARSPLIC 1121 1174
Missing (in isoform II).
FT CONFLICT 385 385
L -> V (IN REF. 2).
FT CONFLICT 618 618
S -> R (IN REF. 2).
FT CONFLICT 653 653
K -> V (IN REF. 2).
FT CONFLICT 779 779
A -> T (IN REF. 2).
FT CONFLICT 1178 1178
D -> S (IN REF. 3).
FT CONFLICT 1196 1201
IRKYM -> SENIICL (IN REF. 3).
SQ SEQUENCE 1257 AA; 142666 MW; F5C0AB6D6ED431DC CRC64;
Query Match 17.1%; Score 72; DB 1; Length 1257;
Best Local Similarity 26.8%; Pred. No. 6.8;
Matches 19; Conservative 21; Mismatches 27; Indels 4; Gaps 2;
QY 13 HLNMSERVWLRKKLQDVHN-FVALGAPLAPRDAGSQRRKKEDNVLVESHEKSLGEANK 71
DB 1179 NMNSTERISFLQEKLEIRKYMYSLKSEVATIDRRKKLKKDREV---SHAGASMSASS 1235
QY 72 ADVNVLTKAS 82
DB 1236 SDTGMSPSSSS 1246
RESULT 10
U225_HSV62
AC U225_HSV62 STANDARD; PRT; 555 AA.
DT 01-OCT-1996 (Rel. 34; Created)
DT 01-OCT-1996 (Rel. 34; Last sequence update)
DT 16-OCT-2001 (Rel. 40; Last annotation update)
DE Virus protein U50.
GN U50 OR KALLR.
OS Human herpesvirus (type 6 / strain 229) (HHV6).
```

```
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Roseolovirus.
OC NCBI_TaxID=36351;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95074921; PubMed=7983761;
RA Stamey F.R., Dominguez G., Black J.B., Dambaugh T.R., Pellett P.E.;
RT "Intragenomic linear amplification of human herpesvirus 6B orILyT
RT suggests acquisition of orILyT by transposition.";
RL J. Virol. 69:589-596(1995).
CC -|- FUNCTION: VIRION PROTEIN.
CC -|- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL25,
CC EHV-1 36, EBV BVRF1, HCMV UL77, ILTV ORF2, AND VZV 34.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF157706; AAB06348.1; -
DR PIR; T44010; T44010.
DR InterPro; IPR002493; UL25.
DR Pfam; PF01499; UL25; 1.
SQ SEQUENCE 555 AA; 63830 MW; 68B86590DC4CD2BC CRC64;
Query Match 16.5%; Score 69.5; DB 1; Length 555;
Best Local Similarity 35.4%; Pred. No. 5;
Matches 23; Conservative 10; Mismatches 27; Indels 5; Gaps 2;
QY 23 LRKKLQDVHNFVALGAPLAPRDAGSQRRKKEDNVLVESHEKSLGEA----NKADVNVLT 78
DB 42 LREKIDQGHDKLLRMRLKTELDALQKMKQSDVLV-NSHLKAIEDALLFTNDGEVNVET 100
QY 79 KAKSQ 83
DB 101 KADTQ 105
RESULT 11
GLMS_FUSNN
ID GLMS_FUSNN STANDARD; PRT; 606 AA.
AC Q8RG65;
DT 28-FEB-2003 (Rel. 41; Created)
DT 28-FEB-2003 (Rel. 41; Last sequence update)
DT 28-FEB-2003 (Rel. 41; Last annotation update)
DE Glucosamine-6-phosphate-6-phosphate aminotransferase [isomerizing]
DE (EC 2.6.1.16) (Hexosephosphate aminotransferase) (D-fructose-6-
DE phosphate amidotransferase) (GPA) (L-glutamine-D-fructose-6-phosphate
DE amidotransferase) (Glucosamine-6-phosphate synthase).
GN GLMS OR FN0452.
OS Fusobacterium nucleatum (subsp. nucleatum).
OC Bacteria; Fusobacteriia; Fusobacteriales; Fusobacteriaceae;
OC Fusobacterium.
OC NCBI_TaxID=76856;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 25586;
RX MEDLINE=21886394; PubMed=11889109;
RA Kapatal V., Anderson I., Ivanova N., Resnik G., Los T., Lykidis A.,
RA Bhattacharya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
RA Vasleva O., Chu L., Kogan Y., Chaga O., Goltzman E., Bernal A.,
RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
RA Fonstein M., Kyripides N., Overbeek R.;
RT "Genome sequence and analysis of the oral bacterium Fusobacterium
RT nucleatum strain ATCC 25586.";
RL J. Bacteriol. 184:2005-2018(2002).
CC -|- FUNCTION: Catalyzes the first step in hexosamine metabolism,
CC converting fructose-6P into glucosamine-6P using glutamine as a
CC nitrogen source (By similarity).
CC -|- CATALYTIC ACTIVITY: L-glutamine + D-fructose 6-phosphate - L-
```

glutamate + D-glucosamine 6-phosphate.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE SIS FAMILY.
 CC -1- SIMILARITY: BELONGS TO THE CLPX CHAPERONE FAMILY. HSLU SUBFAMILY.
 CC -1- SIMILARITY: Contains 1 type-2 glutamine amidotransferase domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AE010357; AAL94648.1;
 CC HAMAP; MF_00164; -; 1.
 CC InterPro; IPR000583; GATase_2.
 CC InterPro; IPR005855; GLMS.
 CC InterPro; IPR001347; SIS.
 CC Pfam; PF003310; GATase_2; 1.
 CC Pfam; PF01380; SIS; 2.
 CC TIGRfams; TIGR01135; glms; 1.
 CC PROSITE; PS00443; GATASE_TYPE_II; 1.
 CC Transferrase; Amidotransferase; Glutamine amidotransferase;
 CC Complete proteome.
 CC INIT_MET 0 0 BY SIMILARITY.
 CC DOMAIN 1 240 GLUTAMINE AMIDOTRANSFERASE.
 CC ACT_SITE 1 1 GATASE (BY SIMILARITY).
 CC ACT_SITE 601 601 ISOMERIZATION FRU-6P (BY SIMILARITY).
 CC SEQUENCE 606 AA; 67768 MW; D6AE271D47D5EA CRC64;
 CC
 CC Query Match 16.1%; Score 68; DB 1; Length 606;
 CC Best Local Similarity 25.6%; Pred. No. 8.1;
 CC Matches 21; Conservative 21; Mismatches 34; Indels 6; Gaps 3;
 CC
 CC QY 1 VSEIQL-HNLGKHLNMSRVERWLRKLDVHNFVALGAPLAPRDAGSORPKKEDNVLV 59
 CC Db 433 ISDLSLKNVNLISEKEKIHDIKIKDKNGFYLGRIDEKVAEGSKMKMEINYI- 491
 CC
 CC QY 60 ESHEKSL--GEANKADVNLTK 79
 CC Db 492 --HTEALPAGELKHGSLALIEK 511
 CC
 CC RESULT 12
 CC ID HSLU_VIBCH STANDARD; PRT; 443 AA.
 CC AC QSKN07;
 CC DT 16-OCT-2001 (Rel. 40, Created)
 CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE ATP-dependent hsl protease ATP-binding subunit hslu.
 CC GN HSLU OR VC2674.
 CC OS Vibrio cholerae.
 CC OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 CC OC Vibrionaceae; Vibrio.
 CC OX NCBI_TaxID=666;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RX STRAIN=El Tor N16961 / Serotype O1;
 CC RX MEDLINE=20406833; Pubmed=10952301;
 CC RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
 CC Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 CC Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 CC Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
 CC McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
 CC Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 CC Fraser C.M.;
 CC RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 CC cholerae.";
 CC RL Nature 406:477-483(2000).
 CC -1- FUNCTION: CHAPERONE SUBUNIT OF A PROTEASOME-LIKE DEGRADATION
 CC COMPLEX (BY SIMILARITY).

-1- SUBUNIT: Interacts with hslv (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE CLPX CHAPERONE FAMILY. HSLU SUBFAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AE004333; AAF95815.1;
 CC PIR; E82046; E82046.
 CC HSP; P32168; IDO2.
 CC TIGR; VC2674; -; 1.
 CC HAMAP; MF_00249; -; 1.
 CC InterPro; IPR003593; AAA_ATPase.
 CC InterPro; IPR003959; AAA_ATPase_Centr.
 CC InterPro; IPR004491; Hsp_HslVU.
 CC Pfam; PF00004; AAA; 1.
 CC SMART; SM00382; AAA; 1.
 CC TIGRfams; TIGR00390; hslu; 1.
 CC KW Chaperone; ATP-binding; Complete proteome.
 CC FT NP_BIND 57 64 ATP (POTENTIAL).
 CC SQ SEQUENCE 443 AA; 49900 MW; DAE13E82FAB6A38F CRC64;
 CC
 CC Query Match 15.9%; Score 67; DB 1; Length 443;
 CC Best Local Similarity 28.8%; Pred. No. 7.3;
 CC Matches 19; Conservative 16; Mismatches 27; Indels 4; Gaps 2;
 CC
 CC QY 13 HLNMSRVERWLRKLDVHNFVALGAPLAPRDAGSORPKKEDNVLVESHEKSL--GEAN 70
 CC Db 112 HQAMEKVKFRAELAEERVDLALLP--PDANGAQAEKSENSSTQVFRKKLRGQLN 169
 CC
 CC QY 71 KADVNV 76
 CC Db 170 DKEIEI 175
 CC
 CC RESULT 13
 CC ID UL25_HSV6G STANDARD; PRT; 378 AA.
 CC AC P52536;
 CC DT 01-OCT-1996 (Rel. 34, Created)
 CC DT 01-OCT-1996 (Rel. 34, Last sequence update)
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
 CC DE Virion protein U50 (Fragment).
 CC GN U50 OR LF3.
 CC OS Human herpesvirus (type 6 / strain GS) (HHV6).
 CC OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 CC OC Betaherpesvirinae; Roseolovirus.
 CC OX NCBI_TaxID=10369;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE=91374623; Pubmed=1654455;
 CC RA Josephs S.F., Ablashi D.V., Salahuddin S.Z., Jagodzinski L.L.,
 CC Wong-Staal F., Gallo R.C.;
 CC RT "Identification of the human herpesvirus 6 glycoprotein H and
 CC putative large tegument protein genes.";
 CC RL J. Virol. 65:5597-5604(1991).
 CC -1- FUNCTION: VIRION PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL25,
 CC EBV-1 36, EBV BVRF1, HCMV UL77, ILTV ORF2, AND VZV 34.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
 CC or send an email to license@isb-sib.ch).
 CC

```
DR EMBL; S57509; AAB19777.1; -.
DR PIR; F56653; F56653.
DR InterPro; IPR002493; UL25.
DR Pfam; PF01499; UL25.1.
FT NONTER 378 378
SQ SEQUENCE 378 AA; 43459 MW; BEB2EF416270AB6 CRC64;

Query Match
Best Local Similarity 15.8%; Score 66.5; DB 1; Length 378;
Matches 22; Conservative 11; Mismatches 27; Indels 5; Gaps 2;

QY 23 LRKKLQDVHNFVALGAPLAPRDSQRPRKKEDNVLVSHESKSLGEA-----NKADVNVLT 78
Db 42 LREKIDQHRDKLLRMRLKLTDLALQKKMQKSDVL-NSHLKAIEDALLFTNDGEVNVET 100

QY 79 KAKSQ 83
Db 101 KADAQ 105

RESULT 14
UL25_HSV6U STANDARD; PRT; 555 AA.
AC PS2387;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Virus protein US0.
GN US0 OR BHRF3.
OS Human herpesvirus (type 6 / strain Uganda-1102) (HRV6).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Roseolovirus.
OX NCBI_TaxID=10370;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92266321; PubMed=7747482;
RA Gompels U.A., Nicholas J., Lawrence G., Jones M., Thomson B.J.,
RA Martin M.E., Efstathiou S., Craxton M., Macaulay H.A.;
RT "The DNA sequence of human herpesvirus-6: structure, coding content,
RT and genome evolution."
RL Virology 209:29-51(1995).
RN [2]
RP SEQUENCE OF 1-378 FROM N.A.
RX MEDLINE=93091236; PubMed=1333836;
RA Gompels U.A., Carrs A.L., Sun N., Arrand J.R.;
RT "Infectivity determinants encoded in a conserved gene block of human
RT herpesvirus-6."
RL DNA Seq. 3:25-39(1992).
CC -!- FUNCTION: VIRION PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL25,
CC EH-V-1 36, EBV BVRF1, HCMV UL77, ILTV ORF2, AND VZV 34.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X83413; CAA58384.1; -.
CC EMBL; X64320; CAA45605.1; -.
CC InterPro; IPR002493; UL25.
CC Pfam; PF01499; UL25; 1.
SQ SEQUENCE 555 AA; 63594 MW; BA0C879FF56130D4 CRC64;

Query Match
Best Local Similarity 15.8%; Score 66.5; DB 1; Length 555;
Matches 22; Conservative 11; Mismatches 27; Indels 5; Gaps 2;

QY 23 LRKKLQDVHNFVALGAPLAPRDSQRPRKKEDNVLVSHESKSLGEA-----NKADVNVLT 78
Db 42 LREKIDQHRDKLLRMRLKLTDLALQKKMQKSDVL-NSHLKAIEDALLFTNDGEVNVET 100
```

```
QY 79 KAKSQ 83
Db 101 KADAQ 105
```

```
RESULT 15
DP04_CLOAB STANDARD; PRT; 396 AA.
AC Q97MB3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA polymerase IV (EC 2.7.7.7) (Pol IV).
GN DINB OR CAC0285.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum."
RL J. Bacteriol. 183:4823-4838(2001).
CC -!- FUNCTION: Poorly processive, error-prone DNA polymerase involved
CC in untargeted mutagenesis. Copies undamaged DNA at stalled
CC replication forks, which arise in vivo from mismatched or
CC misaligned primer ends. These misaligned primers can be extended
CC by polIV. Exhibits no 3'-5' exonuclease (proofreading) activity.
CC May be involved in translesional synthesis, in conjunction with
CC the beta clamp from polIII (By similarity).
CC -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate - N diphosphate
CC + (DNA)(N).
CC -!- COFACTOR: Binds two magnesium ions (By similarity).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -!- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-Y FAMILY.
CC -!- SIMILARITY: Contains 1 unuc domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AE007542; AAK78266.1; -.
CC PIR; G96934; G96934.
CC HAMAP; MF_01113; -.
CC InterPro; IPR001126; UMUC_like.
CC Pfam; PF00817; IMS; 1.
CC PROSITE; PS50173; UMUC; 1.
CC Transferrase; DNA-directed DNA polymerase; DNA replication; DNA repair;
CC DNA-binding; Mutator protein; Magnesium; Complete proteome.
CC DOMAIN 5 192 UMUC.
CC SITE 14 14
CC ACT SITE 112 112 SUBSTRATE DISCRIMINATION (BY SIMILARITY).
CC METAL 9 9 BY SIMILARITY.
CC METAL 111 111 MAGNESIUM (BY SIMILARITY).
CC SEQUENCE 396 AA; 45363 MW; A19826BCBC0D5410 CRC64;

Query Match
Best Local Similarity 15.6%; Score 66; DB 1; Length 396;
Matches 26; Conservative 11; Mismatches 33; Indels 14; Gaps 4;

QY 1 VSEIQLMHNGLKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRD---AGSORPRKKEDNY 57
```

```

Db      :|:|: : || :|: | | :|: | | :|: | |
149 ISTNRLAKHASELNKPKINTLYK-----HEIKDMMPLPVGELEFNVGKMKRK----- 198

QY      | | | | :|: | | | | | | | |
58 LVESHEKSIGEANKADVNVLTRAK 81

Db      | | | | :|: | | | | | | | |
199 LNELHIKTIGELAKYDVNVL-RAK 221

```

Search completed: October 9, 2003, 08:11:21
Job time : 18.1045 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2003, 08:08:56 ; Search time 74.3284 Seconds
(without alignments)
288.159 Million cell updates/sec

Title: US-09-928-048A-4
Perfect score: 422
Sequence: 1 VSEIQLMHNGLKHLNSMERV.....KSLGEANKADVNVLTAKSQ 83

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	368	87.2	86	Q9N1V0	Q9N1V0 equus cabal
2	358	84.8	115	Q9GL67	Q9GL67 felis silve
3	307	72.7	115	Q9Z0L6	Q9Z0L6 mus musculus
4	84	19.9	31	Q91Y90	Q91Y90 peromyscus
5	84	19.9	31	Q91Y91	Q91Y91 peromyscus
6	79.5	18.8	163	Q918E9	Q918E9 figu rubrip
7	78.5	18.6	162	Q918U2	Q918U2 sparus aura
8	73	17.3	565	Q99WC5	Q99WC5 staphylococ
9	72	17.1	140	Q8BYA2	Q8BYA2 mus musculus
10	71	16.8	565	Q8NY08	Q8NY08 staphylococ
11	69	16.4	334	Q8TJX5	Q8TJX5 methanosarc
12	68.5	16.2	256	Q8NRH1	Q8NRH1 drosophila
13	68.5	16.2	256	Q9VDC2	Q9VDC2 drosophila
14	67.5	16.0	271	Q8LMT1	Q8LMT1 oryza sativ
15	67.5	16.0	362	Q8LHC6	Q8LHC6 oryza sativ
16	67.5	16.0	1156	O66878	O66878 aquifex ao

17	67	15.9	674	10	O23544
18	66	15.6	215	5	O17915
19	66	15.6	341	17	Q97CE4
20	66	15.6	886	10	Q8W3D7
21	66	15.6	896	10	Q8W3D7
22	66	15.6	1175	10	Q8SHT1
23	66	15.6	1205	10	Q8S8B4
24	65.5	15.5	449	4	Q8H2D2
25	65.5	15.5	823	16	Q8N2Q8
26	65.5	15.5	861	10	Q8PBY4
27	65	15.4	189	11	Q9AVZ9
28	65	15.4	238	11	Q922S6
29	65	15.4	283	9	Q8BYB0
30	65	15.4	283	9	Q9AZW5
31	65	15.4	377	5	Q9CFN5
32	65	15.4	398	11	Q9XR80
33	65	15.4	455	11	Q8BXV6
34	65	15.4	873	4	Q9NYU3
35	65	15.4	1226	4	Q9NZB6
36	65	15.4	1228	11	Q9JKB5
37	64.5	15.3	264	13	Q9PS76
38	64.5	15.3	292	13	Q9PS77
39	64.5	15.3	321	5	Q94940
40	64.5	15.3	495	4	Q9NUP4
41	64.5	15.3	495	4	Q8NEH6
42	64.5	15.3	495	4	Q8IYT6
43	64.5	15.3	792	13	O13110
44	64.5	15.3	1018	3	Q9UST0
45	64.5	15.3	1118	13	Q98951

ALIGNMENTS

RESULT 1

Q9N1V0 PRELIMINARY; PRT; 86 AA.
ID Q9N1V0
AC Q9N1V0
DT 01-OCT-2000 (TREMREL. 15, Created)
DT 01-OCT-2000 (TREMREL. 15, Last sequence update)
DT 01-JUN-2002 (TREMREL. 21, Last annotation update)
DE Parathyroid hormone (Fragment).
GN PTH.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20082971; PubMed=10613847;
RA Caetano A.R., Shue Y.L., Lyons L.A., O'Brien S.J., Laughlin T.F.,
RA Bowling A.T., Murray J.D.;
RT "A comparative gene map of the horse (Equus caballus).";
RL Genome Res. 9:1239-1249(1999).
DR EMBL: AF134233; RAF62347.1; .
DR HSSP: P01270; IHPY.
DR InterPro: IPR001415; Parathyrd_hrm.
DR InterPro: IPR003625; Pthyrhorm_sub.
DR Pfam: PF01279; Parathyroid; 1.
DR ProDom: PD010687; Pthyrhorm_sub; 1.
DR SMART: SM00087; PTH; 1.
DR PROSITE: PS00335; PARATHYROID; 1.
FT NON_TER
SQ SEQUENCE 86 AA; 9805 MW; 253184EA681A2022 CRC64;

Query Match 87.2%; Score 368; DB 6; Length 86;

Best Local Similarity 84.3%; Pred. No. 2.2e-33;

Matches 70; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 VSEIQLMHNGLKHLNSMERVWLRLKLDVHNFVALGAPLRDAGSORPKKEDNVLVE 60

DB 4 VSEIQLMHNGLKHLNSMERVWLRLKLDVHNFVALGAPLRDAGSORPKKEDNVLVE 63

Qy 61 SHEKSLGEANKADVNLTKAKSQ 83
||: ||||: ||||: ||: ||||
Db 64 SHQXSLGEADKADVLSKTKSQ 86

RESULT 2

Q9GL67	ID	Q9GL67	PRELIMINARY;	PRT;	115 AA.
Q9GL67	AC	Q9GL67			
Q9GL67	DT	01-WAR-2001	(TremBrel, 16, Created)		
Q9GL67	DT	01-MAR-2001	(TremBrel, 16, Last sequence update)		
Q9GL67	DT	01-JUN-2002	(TremBrel, 21, Last annotation update)		
Q9GL67	DE	Preproparathyroid hormone precursor.			
Q9GL67	GN	PTH			

OS *Felis silvestris catus* (Cat).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OC NCBI_TaxId=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Toribio R.E., Kohn C.W., Leone G.W., Capen C.C., Rosol T.J.;
 RL "Molecular cloning of feline preproarthyroid hormone."
 RT Submitted (Oct-2000) to the EMBL/GenBank/DBJ databases.

DR	EMBL; AF309967; AAG30545.1; -.
DR	HSP; P01368; 1ZWC.
DR	InterPro; IPR001415; Parathyrd_hrm.
DR	InterPro; IPR003625; Pthyrohm_sub.
DR	Fam; PF01279; Parathyroid; 1.
DR	ProDom; PDO10687; Pthyrohm_sub; 1.
DR	SMART; SM0087; PTH; 1.
DR	PROSITE; PS00335; PARATHYROID; 1.
KW	Signal.
FT	SIGNAL. 1 25
FT	CHAIN 32 115
FT	PARATHYROID HORMONE.
SQ	SEQUENCE 115 AA; 12921 MW; 80CDS57CC6A1A47E CRC64;

```

Query Match      84.8%; Score 358; DB 6; Length 115;
Best Local Similarity 83.13; Pred. No. 3.9e-32;
Matches 69; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 VSEIQLMHNIGKHLNSMERYEWLRKIQDVHNFVALGAPLAPRDAGSORPKKEDNVLVE 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 33 VSEIQFMHNIGKHLSSVRYEWLRKIQDVHNFVALGAPIAHRDGGSPRKKEDNVPAE 92
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 SHEXSLGEANKADYNYLTAKSQ 83
      :||:|||||:||||:|||||
db 93 NHQKSLGEADKADYDVLIRAKSQ 115
      :||:|||||:||||:|||||

```

RESULT 3

Q9Z0L1	Q9Z0L2	Q9Z0L3	Q9Z0L4	Q9Z0L5	Q9Z0L6	Q9Z0L7	Q9Z0L8	Q9Z0L9	Q9Z0L10	Q9Z0L11	Q9Z0L12	Q9Z0L13	Q9Z0L14	Q9Z0L15	Q9Z0L16	Q9Z0L17	Q9Z0L18	Q9Z0L19	Q9Z0L20	Q9Z0L21	Q9Z0L22	Q9Z0L23	Q9Z0L24	Q9Z0L25	Q9Z0L26	Q9Z0L27	Q9Z0L28	Q9Z0L29	Q9Z0L30	Q9Z0L31	Q9Z0L32	Q9Z0L33	Q9Z0L34	Q9Z0L35	Q9Z0L36	Q9Z0L37	Q9Z0L38	Q9Z0L39	Q9Z0L40	Q9Z0L41	Q9Z0L42	Q9Z0L43	Q9Z0L44	Q9Z0L45	Q9Z0L46	Q9Z0L47	Q9Z0L48	Q9Z0L49	Q9Z0L50	Q9Z0L51	Q9Z0L52	Q9Z0L53	Q9Z0L54	Q9Z0L55	Q9Z0L56	Q9Z0L57	Q9Z0L58	Q9Z0L59	Q9Z0L60	Q9Z0L61	Q9Z0L62	Q9Z0L63	Q9Z0L64	Q9Z0L65	Q9Z0L66	Q9Z0L67	Q9Z0L68	Q9Z0L69	Q9Z0L70	Q9Z0L71	Q9Z0L72	Q9Z0L73	Q9Z0L74	Q9Z0L75	Q9Z0L76	Q9Z0L77	Q9Z0L78	Q9Z0L79	Q9Z0L80	Q9Z0L81	Q9Z0L82	Q9Z0L83	Q9Z0L84	Q9Z0L85	Q9Z0L86	Q9Z0L87	Q9Z0L88	Q9Z0L89	Q9Z0L90	Q9Z0L91	Q9Z0L92	Q9Z0L93	Q9Z0L94	Q9Z0L95	Q9Z0L96	Q9Z0L97	Q9Z0L98	Q9Z0L99	Q9Z0L100	Q9Z0L101	Q9Z0L102	Q9Z0L103	Q9Z0L104	Q9Z0L105	Q9Z0L106	Q9Z0L107	Q9Z0L108	Q9Z0L109	Q9Z0L110	Q9Z0L111	Q9Z0L112	Q9Z0L113	Q9Z0L114	Q9Z0L115	Q9Z0L116	Q9Z0L117	Q9Z0L118	Q9Z0L119	Q9Z0L120	Q9Z0L121	Q9Z0L122	Q9Z0L123	Q9Z0L124	Q9Z0L125	Q9Z0L126	Q9Z0L127	Q9Z0L128	Q9Z0L129	Q9Z0L130	Q9Z0L131	Q9Z0L132	Q9Z0L133	Q9Z0L134	Q9Z0L135	Q9Z0L136	Q9Z0L137	Q9Z0L138	Q9Z0L139	Q9Z0L140	Q9Z0L141	Q9Z0L142	Q9Z0L143	Q9Z0L144	Q9Z0L145	Q9Z0L146	Q9Z0L147	Q9Z0L148	Q9Z0L149	Q9Z0L150	Q9Z0L151	Q9Z0L152	Q9Z0L153	Q9Z0L154	Q9Z0L155	Q9Z0L156	Q9Z0L157	Q9Z0L158	Q9Z0L159	Q9Z0L160	Q9Z0L161	Q9Z0L162	Q9Z0L163	Q9Z0L164	Q9Z0L165	Q9Z0L166	Q9Z0L167	Q9Z0L168	Q9Z0L169	Q9Z0L170	Q9Z0L171	Q9Z0L172	Q9Z0L173	Q9Z0L174	Q9Z0L175	Q9Z0L176	Q9Z0L177	Q9Z0L178	Q9Z0L179	Q9Z0L180	Q9Z0L181	Q9Z0L182	Q9Z0L183	Q9Z0L184	Q9Z0L185	Q9Z0L186	Q9Z0L187	Q9Z0L188	Q9Z0L189	Q9Z0L190	Q9Z0L191	Q9Z0L192	Q9Z0L193	Q9Z0L194	Q9Z0L195	Q9Z0L196	Q9Z0L197	Q9Z0L198	Q9Z0L199	Q9Z0L200	Q9Z0L201	Q9Z0L202	Q9Z0L203	Q9Z0L204	Q9Z0L205	Q9Z0L206	Q9Z0L207	Q9Z0L208	Q9Z0L209	Q9Z0L210	Q9Z0L211	Q9Z0L212	Q9Z0L213	Q9Z0L214	Q9Z0L215	Q9Z0L216	Q9Z0L217	Q9Z0L218	Q9Z0L219	Q9Z0L220	Q9Z0L221	Q9Z0L222	Q9Z0L223	Q9Z0L224	Q9Z0L225	Q9Z0L226	Q9Z0L227	Q9Z0L228	Q9Z0L229	Q9Z0L230	Q9Z0L231	Q9Z0L232	Q9Z0L233	Q9Z0L234	Q9Z0L235	Q9Z0L236	Q9Z0L237	Q9Z0L238	Q9Z0L239	Q9Z0L240	Q9Z0L241	Q9Z0L242	Q9Z0L243	Q9Z0L244	Q9Z0L245	Q9Z0L246	Q9Z0L247	Q9Z0L248	Q9Z0L249	Q9Z0L250	Q9Z0L251	Q9Z0L252	Q9Z0L253	Q9Z0L254	Q9Z0L255	Q9Z0L256	Q9Z0L257	Q9Z0L258	Q9Z0L259	Q9Z0L260	Q9Z0L261	Q9Z0L262	Q9Z0L263	Q9Z0L264	Q9Z0L265	Q9Z0L266	Q9Z0L267	Q9Z0L268	Q9Z0L269	Q9Z0L270	Q9Z0L271	Q9Z0L272	Q9Z0L273	Q9Z0L274	Q9Z0L275	Q9Z0L276	Q9Z0L277	Q9Z0L278	Q9Z0L279	Q9Z0L280	Q9Z0L281	Q9Z0L282	Q9Z0L283	Q9Z0L284	Q9Z0L285	Q9Z0L286	Q9Z0L287	Q9Z0L288	Q9Z0L289	Q9Z0L290	Q9Z0L291	Q9Z0L292	Q9Z0L293	Q9Z0L294	Q9Z0L295	Q9Z0L296	Q9Z0L297	Q9Z0L298	Q9Z0L299	Q9Z0
--------	--------	--------	--------	--------	--------	--------	--------	--------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	---------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	----------	------

FN	PIH.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;	
OX	NCBI_TaxID=10090;	
RN	[1]	

RP	SEQUENCE FROM N.A.
RC	STRAIN-129/SV;
RA	Karaplis A.C., He B., Hlou-Tim F.T., Al-Akad B., Kronenberg H.M.
RT	"Cloning of the murine gene encoding parathyroid hormones: genomic
RT	organization and nucleotide sequence."
RT	Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RL	EMBL: AF065075; AAC9656.1; -
DR	HSSP: P01270; IZWB.
DR	MGI: 977999; Pth.
DR	InterPro: IPR001415; Parathyrd_hrm.

DR InterPro: IPR003625; Pthyhorm_sub.
DR Pfam: PF01279; Parathyroid; 1.
DR ProDom: PD010687; Pthyhorm_sub; 1.
DR SMART: SM00087; PTH; 1.
DR PROSITE: PS00335; PARATHYROID; 1.

KW	SIGNAL.		
FT	SIGNAL	1	25
FT	CHAIN	32	115
SQ	SEQUENCE	115 AA;	13825 MW; DA43FABBCB4E2FD9 CRC64;

QY	1	VSEIQLMHNGLKHLNSMERYEWLRRKKLQDVHNFVALGAPLAPRADA
Db	33	VSEIQLMHNGLKHLASMERQWLRRKLQDMHNFVSLGVQMAARDG
QY	61	SHEKSLGEANKADYNYLTKAKSO 83
Db	93	GNPKSLGEGKADVDLVVKKSQ 115

RESULT 4

Q91Y90	PRELIMINARY;	PRT;	31 AA.
ID	Q91Y90		
AC	Q91Y90		
DT	01-DEC-2001	(TREMBLrel. 19, Created)	
DT	01-DEC-2001	(TREMBLrel. 19, Last sequence update)	
DT	01-OCT-2002	(TREMBLrel. 22, Last annotation update)	
DE	Parathyroid hormone (Fragment).		

GN PTH.
OS *Peromyscus maniculatus* (Deer mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC *Peromyscus*.

OX		NCBI_TaxID=10042;	
RN	[1]	SEQUENCE FROM N.A.	
RP		Prime K.L., Dewey M.J.;	
RA		Submitted (May-2001) to the EMBL/GenBank/DDBJ databases.	
RL		EMBL; AF382953; AAKG3072.1;	
DR		InterPro; IPR001415; Parathyroid hrm.	
DR		InterPro; IPR003625; Pthyrrhorm_sub.	
DR		Pfam; PF01279; Parathyroid; 1.	
DR		ProDom; PD010687; Pthyrrhorm_sub; 1.	
DR		PROSITE; PS00335; PARATHYROID; 1.	
FT		NON_TER	1
FT		NON_TER	31
FT		SEQUENCE	31 AA; 3461 MW; A208B0E772B9B55B CRC64:
SQ			

Qy. 1 VSEIQLMHNLGKHLNSME 18
 14 VSEIQLMHNLGKHLASME 31
 Db

RESULT 5

Q91Y91	PRELIMINARY;	PRT;	31 AA.
ID Q91Y91			
AC Q91Y91			
DT 01-DEC-2001	(TREMBlrel. 19, Created)		
DT 01-DEC-2001	(TREMBlrel. 19, Last sequence update)		
DT 01-OCT-2002	(TREMBlrel. 22, Last annotation update)		
DE Parathyroid hormone (Fragment).			
CN PTH			

OC
 OC Peromyscus pollomotus (oldfield mouse).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
 OC Peromyscus.

```

OX NCBI_TaxID=42413;
RN [1]
RP SEQUENCE FROM N.A.
RA Prince K.L., Devey M.J.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF382952; AAK63071.1;
DR InterPro; IPR001415; Parathyrd_hrm.
DR Pfam; PF01279; Parathyroid; 1.
DR ProDom; PD010687; Pthyrhorm_sub; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
FT NON_TER 1
FT NON_TER 31
SQ SEQUENCE 31 AA; 3461 MW; A208B0E772B9B55B CRC64;

Query Match 19.8%; Score 84; DB 11; Length 31;
Best Local Similarity 94.4%; Pred. No. 0.024;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VSEIQLMHNGLKHLNSME 18
DB 14 VSEIQLMHNGLKHLASME 31

RESULT 6
Q918E9 PRELIMINARY; PRT; 163 AA.
AC Q918E9
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DE 01-MAR-2003 (Tremblrel. 23, Last annotation update)
GN PTHRP.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RA Power D.M., Flannigan J., Ingleton P.M., Canario A.V.M., Danks J.,
RA Elgar G., Clark M.S.;
RT "Genomic structure and expression of parathyroid hormone-related
RT protein in a teleost, Fugu rubripes."
RL Gene 250:67-75(2000).
DR EMBL; AJ249391; CAB94712.1;
DR HSSP; P12272; 1B2G.
DR InterPro; IPR001415; Parathyrd_hrm.
DR Pfam; PF01279; Parathyroid; 1.
DR ProDom; PD013225; PTH_related; 1.
KW SIGNAL.
FT SIGNAL 1 34 POTENTIAL.
SQ SEQUENCE 163 AA; 18698 MW; 3AC5F2C764732278 CRC64;

Query Match 18.8%; Score 79.5; DB 13; Length 163;
Best Local Similarity 27.3%; Pred. No. 0.53;
Matches 30; Conservative 10; Mismatches 35; Indels 35; Gaps 4;

QY 1 VSEIQLMHNGLKHLNSMERVLRKLDVHNFVALGAPLAPRDAGSQRPKKEDNVLVE 60
DB 39 VSHAQLMHDKRSLOEFRMRWLKLEEVH-----ANEAPPVQSRQTQTQTSFN 90
QY 61 S-HKSLG-----EANKA-----DVNVLTKAKSQ 83
DB 91 SLHEKPPGATKNLPDRFSLDREGTNLPQETNKALAYKDQPLKATRKKK 140

RESULT 7
Q918U2 PRELIMINARY; PRT; 162 AA.
ID Q918U2

```

```

AC Q918U2; 2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Parathyroid hormone-related protein.
GN PTHRP.
OS Sparus aurata (Gilthead sea bream).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Sparidae; Sparus.
OX NCBI_TaxID=8175;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=20304721; PubMed=10843788;
RA Flanagan J.A., Power A.V., Danks J.A., Brown B.L., Ingleton P.M.;
RA Clark M.S., Canario A.V., Danks J.A., Brown B.L., Ingleton P.M.;
RT "Cloning of the cDNA for sea bream (Sparus aurata) parathyroid
RT hormone-related protein."
RL Gen. Comp. Endocrinol. 118:373-382(2000).
DR EMBL; AF197904; AAF79073.1;
DR HSSP; P12272; 1B2G.
DR InterPro; IPR001415; Parathyrd_hrm.
DR ProDom; PD013225; PTH_related; 1.
DR Pfam; PF01279; Parathyroid; 1.
DR ProDom; PD013225; PTH_related; 1.
SQ SEQUENCE 162 AA; 18722 MW; 5E8D5E07F9F5EDC9 CRC64;

Query Match 18.6%; Score 78.5; DB 13; Length 162;
Best Local Similarity 28.4%; Pred. No. 0.68;
Matches 31; Conservative 11; Mismatches 32; Indels 35; Gaps 5;

QY 1 VSEIQLMHNGLKHLNSMERVLRKLDVHNFVALGAPLAPRDAGSQRPKKEDNVLVE 60
DB 39 VSHAQLMHDKRSLOEFRMRWLKLEEVH-----TADDRVQSR-----TQSTFSGNAL-- 90
QY 61 SHEKSLG-----EANKA-----DVNVLTKAKSQ 83
DB 91 HEKPPGATKNLPDRFSLDREGTNLPQETNKALAYKDQPLKATRKKK 138

RESULT 8
Q99WC5 PRELIMINARY; PRT; 565 AA.
ID Q99WC5
AC Q99WC5
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DE 01-MAR-2003 (Tremblrel. 23, Last annotation update)
GN DNA polymerase III gamma and tau subunits.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699), and
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878; 158879;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cul L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mitutani T. Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Saito K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240(2001).
DR EMBL; AP003359; BAB56640.1;
DR EMBL; AP003130; BAB41666.1;
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003593; AAA_ATPase_cent.

```

```

DR InterPro: IPR001270; Chaprin-clpA/B.
DR InterPro: IPR000345; CytC_heme_bind.
DR InterPro: IPR000463; Fatty_acid_BP.
DR InterPro: IPR000862; RFCdomain.
DR Pfam: PF00004; AAA_1.
DR PRINTS: PR00300; CLPPROTEASEA.
DR SMART: SM00382; AAA; 1.
DR PROSITE: PS00190; CYTOCHROME_C; 1.
DR PROSITE: PS00214; FAPB; 1.
KW Complete proteome.
SQ SEQUENCE 565 AA; 63471 MW; F29A7F07095F02AA CRC64;

Query Match 17.3%; Score 73; DB 16; Length 565;
Best Local Similarity 29.4%; Pred. No. 12;
Matches 20; Conservative 15; Mismatches 23; Indels 10; Gaps 2

Qy 14 LNSMERVEWLRLKLDVHNEFVALGAPLAPRDAGSQRP-----RYKEDNVLVESHEKSLGEA 69
Db 376 LQRMQEQE-----QELTKLQAGVSVAPOAKSKKPGRIQSKNAFMSQGIATKAYLDKA 429
Qy 70 NKADNVNL 77
Db 430 NKADIKLL 437

RESULT 9
Q8BYA2 PRELIMINARY; PRT; 140 AA.
ID Q8BYA2 AC Q8BYA2;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Retinoblastoma-binding protein 1 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN genome Exploration Research Group Phase I & II Team;
RT *Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.*;
RL Nature 420:563-573(2002).
DR ENBL: AK041444; BAC30948.1; -.
FT NON_TER 1
SQ SEQUENCE 140 AA; 15988 MW; 15CE80236A5E9930 CRC64;

Query Match 17.1%; Score 72; DB 11; Length 140;
Best Local Similarity 26.8%; Pred. No. 3;
Matches 19; Conservative 21; Mismatches 27; Indels 4; Gaps 2

Qy 13 HLSMERVEWLRLKLDVHNEFVALGAPLAPRDAGSQRPKRKEDNVLVESHEKSLGEANK 71
Db 62 NNNSTERISFLOEKIQEIRKYMYSLKSEVATIDRRKRRLKKKQREV--SHAGASMSAS 118
Qy 72 ADVNVLTRAKS 82
Db 119 SDTGMSPSSSS 129.

RESULT 10
Q8NY08 PRELIMINARY; PRT; 565 AA.
ID Q8NY08 AC Q8NY08;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE DNA polymerase III gamma and tau subunits.
GN DNAX OR MW0433.
OS Staphylococcus aureus (strain MW2).

```

RESULT 14
Q8LMT1

```
QY      58 -----LIVESHEKSLGEANKADVNLTKAKSO 83  
DB     175 NDATPDGPTDVTIVKKRGKHKSQQIKSPESPAGOSTRDPVTTAAPAKSE 226
```

Search completed: October 9, 2003, 08:13:31
Job time : 77.3284 secs

ID	Q8LMT1	PRELIMINARY;	PRT;	271 AA.
AC	Q8LMT1;			
DT	01-OCT-2002 (TReMBLrel. 22, Created)			
DT	01-OCT-2002 (TReMBLrel. 22, Last sequence update)			
DT	01-MAR-2003 (TReMBLrel. 23, Last annotation update)			
DE	Putative polyprotein, 3'-partial (Fragment).			
GN	OSJNBA0079H13.1			
OS	Oryza sativa (japonica cultivar-group).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;			
OC	Ehrhartoideae; Oryzeae; Oryza.			
OX	NCBI_TaxID=39947;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Nipponbare;			
RA	Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,			
RA	Overton II L.L., Bera J.J., Tsirlin T., Krol M.I., Jarrahi B.B.,			
RA	Jin S.S., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S.,			
RA	Uterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B.,			
RA	Peterson J.J., Quackenbush J., White C., Salzberg S.L., Fraser C.M.;			
RT	*Oryza sativa chromosome 10 BAC OSJNBA0079H13 genomic sequence.*;			
RL	Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: AC104616; AAM54142.1;			
DR	Gramene; Q8LMT1;			
KW	Polyprotein.			
FT	NON_TER	271	271	
SQ	SEQUENCE	271 AA;	29864 MW;	91372974301F296A CRC64;
	Query Match	16.08;	Score 67.5;	DB 10; Length 271;
	Best Local Similarity	27.38;	Pred. No. 21;	
	Matches	27;	Conservative	19; Mismatches 32; Indels 21; Gaps -4;
QY	1	VSETQLMHNGLKHLNSMERVFWLR	-----KKIQDVHNFVALG	-----APLAPRDAGS 47
DB	44	LDNVALVENLKYNNLSVSQILWRLMCCSRKLE	-----VRLGHVGFDHLRLSGSLDVR	98
QY	48	QRPRKKEDNVLES	---HEKSLGANKADNVNLTAKSQ	83
DB	99	GLPKLKKDLDLVCSPCRHKMKVASSRTPIVSVMTDAPGQ	137	
RESULT 15				
ID	Q8LHC6	PRELIMINARY;	PRT;	362 AA.
AC	Q8LHC6;			
DT	01-OCT-2002 (TReMBLrel. 22, Created)			
DT	01-OCT-2002 (TReMBLrel. 22, Last sequence update)			
DT	01-MAR-2003 (TReMBLrel. 23, Last annotation update)			
DE	P0458E05.24 protein.			
GN	P0458E05.24			
OS	Oryza sativa (japonica cultivar-group).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;			
OC	Ehrhartoideae; Oryzeae; Oryza.			
OX	NCBI_TaxID=39947;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Nipponbare;			
RA	Sasaki T., Matsumoto T., Yamamoto K.;			
RT	*Oryza sativa Nipponbare(GA3) genomic DNA, chromosome 1, PAC			
RT	clone:P0458E05.*;			
RL	Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: AP004365; BAC05624.1;			
DR	Gramene; Q8LHC6;			
SQ	SEQUENCE	362 AA;	39366 MW;	B87DEB28851E6740 CRC64;
	Query Match	16.04;	Score 67.5;	DB 10; Length 362;
	Best Local Similarity	20.54;	Pred. No. 29;	
	Matches	23;	Conservative	21; Mismatches 37; Indels 31; Gaps 3;
QY	1	VSETQLMHNGLKHLNSMERVFWLRKKIQD	-VHNFVALGAPLAPRDAGSQRPKKEDNV	-- 57
DB	117	LSEHLRLNLCNGPFAEKDGLAKYKLVLPNLRIFS	--KPMVSAKSKNSKNSENLP1	174

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2003, 08:08:57 ; Search time 21.0597 Seconds
(without alignments)
166.755 Million cell updates/sec

Title: US-09-928-048A-4
Perfect score: 422
Sequence: 1 VSEIQLMHNGLKHLNSMERY.....KSLGEANKADVNLTAKSQ 83

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:*
- 1: /cgn2_6/ptodata/1/iaa/5A-COMB.pep:*
 - 2: /cgn2_6/ptodata/1/iaa/5B-COMB.pep:*
 - 3: /cgn2_6/ptodata/1/iaa/6A-COMB.pep:*
 - 4: /cgn2_6/ptodata/1/iaa/6B-COMB.pep:*
 - 5: /cgn2_6/ptodata/1/iaa/PCTUS-COMB.pep:*
 - 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	417	98.8	83	4	US-10-002-818-2
2	417	98.8	84	1	US-07-863-014-2
3	417	98.8	84	1	US-08-332-453-2
4	417	98.8	84	1	US-08-689-190-2
5	417	98.8	84	2	US-08-835-231-9
6	417	98.8	84	2	US-08-805-918-3
7	417	98.8	84	3	US-09-108-661-9
8	417	98.8	84	4	US-10-002-818-1
9	417	98.8	84	5	PCT-US95-15800-25
10	412	97.6	84	2	US-08-142-551B-1
11	412	97.6	84	2	US-08-411-726-1
12	407	96.4	84	1	US-07-707-114-1
13	368	87.2	84	1	US-07-773-098-2
14	364	86.3	84	2	US-08-733-446-5
15	359	85.1	84	1	US-07-773-098-1
16	356	84.4	81	2	US-08-733-446-4
17	352	83.4	84	1	US-07-776-272-14
18	351	83.2	80	2	US-08-733-446-3
19	350	82.9	84	1	US-07-773-098-9
20	350	82.9	84	1	US-07-773-098-10
21	347	82.2	79	2	US-08-733-446-2
22	342	81.0	78	2	US-08-733-446-1
23	341	80.8	84	1	US-07-773-098-7
24	341	80.8	84	1	US-07-773-098-8
25	337	79.9	84	3	US-09-044-536A-36
26	337	79.9	84	3	US-09-044-536A-7
27	248	58.8	51	4	US-10-002-818-3

28	237	56.2	50	2	US-08-142-551B-119	Sequence 119, Appl
29	193	45.7	38	1	US-08-112-024-1	Sequence 1, Appli
30	193	45.7	38	1	US-08-232-849-1	Sequence 1, Appli
31	193	45.7	38	2	US-08-625-586-1	Sequence 1, Appli
32	193	45.7	38	3	US-09-128-401-1	Sequence 1, Appli
33	187	44.3	37	1	US-08-440-117-1	Sequence 1, Appli
34	187	44.3	37	3	US-09-088-738A-16	Sequence 16, Appli
35	186	44.1	38	5	PCT-US95-15800-29	Sequence 29, Appli
36	183	43.4	36	1	US-08-256-363-4	Sequence 4, Appli
37	179	42.4	34	1	US-08-256-363-2	Sequence 2, Appli
38	179	42.4	35	1	US-08-256-363-3	Sequence 3, Appli
39	179	42.4	36	1	US-08-112-024-2	Sequence 2, Appli
40	175	41.5	33	1	US-08-256-363-1	Sequence 1, Appli
41	175	41.5	34	1	US-07-765-373-1	Sequence 1, Appli
42	175	41.5	34	1	US-08-033-099-1	Sequence 1, Appli
43	175	41.5	34	1	US-08-262-495C-1	Sequence 1, Appli
44	175	41.5	34	1	US-07-915-247A-1	Sequence 1, Appli
45	175	41.5	34	1	US-08-443-863-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-10-002-818-2
; Sequence 2, Application US/10002818
; Patent No. 6524788
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas L.
; TITLE OF INVENTION: Methods for Monitoring Therapeutic Suppression of Parathyroidism
; TITLE OF INVENTION: Renal Patients Having Secondary Hyperparathyroidism
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/002.818
; CURRENT FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Microsoft Word 2000 - ASCII format
; SEQ ID NO 2
; LENGTH: 83
; TYPE: PRT
; ORGANISM: human parathyroid hormone peptide fragment
US-10-002-818-2

Query Match 98.8%; Score 417; DB 4; Length 83;
Best Local Similarity 98.8%; Pred. No. 1.8e-44;
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	1	VSEIQLMHNGLKHLNSMERYEWLKKLQDVHNFVALGAPLAPRDAGSORPKKEDNVLVE	60
Db	1	VSEIQLMHNGLKHLNSMERYEWLKKLQDVHNFVALGAPLAPRDAGSORPKKEDNVLVE	60
Qy	61	SHEKSLGEANKADVNLTAKSQ	83
Db	61	SHEKSLGEANKADVNLTAKSQ	83

RESULT 2

US-07-863-014-2
; Sequence 2, Application US/07863014
; Patent No. 5382658
; GENERAL INFORMATION:
; APPLICANT: KRONIS, K. Anne
; APPLICANT: BOZZATO, Richard P.
; TITLE OF INVENTION: STABILITY-ENHANCED VARIANTS OF PARATHYROID HORMONE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/863,014
FILING DATE: 19920403
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16777/163 ALLE
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-863-014-2

Query Match 98.8%; Score 417; DB 1; Length 84;
Best Local Similarity 98.8%; Pred. No. 1.8e-44;
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 VSEIOLMHLNGLKHLNSMERVWLKRLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE 60
Db 2 VSEIOLMHLNGLKHLNSMERVWLKRLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE 61
QY 61 SHEKSLGEANKADVNVLTAKSQ 83
Db 62 SHEKSLGEANKADVNVLTAKSQ 84

RESULT 3
US-08-332-453-2
Sequence 2, Application US/08332453
Patent No. 559792
GENERAL INFORMATION:
APPLICANT: KRONIS, K. Anne
APPLICANT: BOZZATO, Richard P.
TITLE OF INVENTION: BONE-STIMULATING, NON-VASOACTIVE
TITLE OF INVENTION: PARATHYROID HORMONE VARIANTS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,453
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/900,680
FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16777/182 ALLE
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109

TELEX: 899149
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-453-2

Query Match 98.8%; Score 417; DB 1; Length 84;
Best Local Similarity 98.8%; Pred. No. 1.8e-44;
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 VSEIOLMHLNGLKHLNSMERVWLKRLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE 60
Db 2 VSEIOLMHLNGLKHLNSMERVWLKRLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE 61
QY 61 SHEKSLGEANKADVNVLTAKSQ 83
Db 62 SHEKSLGEANKADVNVLTAKSQ 84

RESULT 4
US-08-689-190-2
Sequence 2, Application US/08689190
Patent No. 5714349
GENERAL INFORMATION:
APPLICANT: FUKUDA, Tsunehiko
APPLICANT: OSHIKA, Yuri
APPLICANT: YAMADA, Takao
TITLE OF INVENTION: SYNTHETIC GENE CODING FOR HUMAN
TITLE OF INVENTION: PARATHYROID HORMONE
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
STREET: 130 Water Street
CITY: Boston
STATE: Massachusetts
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/689,190
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/006,197
FILING DATE:
APPLICATION NUMBER: US/08/016,171
FILING DATE:
APPLICATION NUMBER: US/07/765,371
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, Gregory D.
REGISTRATION NUMBER: 30,901
REFERENCE/DOCKET NUMBER: 41,288
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-689-190-2

Query Match 98.8%; Score 417; DB 1; Length 84;

Best Local Similarity 98.8%; Pred. No. 1.8e-44;
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVYLE 60
|||||
Db 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVYLE 61
|||||
QY 61 SHEKSLGEANKADVNLTKAKSQ 83
|||||
Db 62 SHEKSLGEADKADVNLTKAKSQ 84
|||||

RESULT 5

US-08-835-231-9
; Sequence 9, Application US/08835231
; Patent No. 5861284
; GENERAL INFORMATION:
; APPLICANT: NISHIMURA, Osamu
; APPLICANT: KURIYAMA, Masato
; APPLICANT: KOYAMA, No. 5861284uyuk1
; APPLICANT: FUKUDA, Tsunehiko
; TITLE OF INVENTION: METHOD FOR PRODUCING A BIOLOGICALLY
; TITLE OF INVENTION: ACTIVE RECOMBINANT CYSTEINE-FREE
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/835,231
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/350,709
; FILING DATE: 07-DEC-1994
; APPLICATION NUMBER: 07/838,857
; FILING DATE: 18-FEB-1992
; APPLICATION NUMBER: JP 024841
; FILING DATE: 19-FEB-1991
; APPLICATION NUMBER: JP 0271438
; FILING DATE: 18-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 41614-FWC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
US-08-835-231-9

Query Match 98.8%; Score 417; DB 2; Length 84;
Best Local Similarity 98.8%; Pred. No. 1.8e-44;
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVYLE 60
|||||
Db 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVYLE 61
|||||
QY 61 SHEKSLGEANKADVNLTKAKSQ 83
|||||
Db 62 SHEKSLGEADKADVNLTKAKSQ 84
|||||

RESULT 6

US-08-805-918-3
; Sequence 3, Application US/08805918
; Patent No. 5885821
; GENERAL INFORMATION:
; APPLICANT: MAGOTA, Koji
; APPLICANT: MASUDA, Toyofumi
; APPLICANT: SUZUKI, Yuji
; APPLICANT: YABUTA, Masayuki
; TITLE OF INVENTION: PROCESS FOR PRODUCTION OF SECRETORY KEX2
; TITLE OF INVENTION: DERIVATIVES
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/805,918
; FILING DATE: 04-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-073217
; FILING DATE: 04-MAR-1996
; APPLICATION NUMBER: JP 8-352580
; FILING DATE: 16-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M.
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 001560-295
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-805-918-3

Query Match 98.8%; Score 417; DB 2; Length 84;
Best Local Similarity 98.8%; Pred. No. 1.8e-44;
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVYLE 60
|||||
Db 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVYLE 61
|||||
QY 61 SHEKSLGEANKADVNLTKAKSQ 83
|||||
Db 62 SHEKSLGEADKADVNLTKAKSQ 84
|||||

RESULT 7

US-09-108-661-9
; Sequence 9, Application US/09108661
; Patent No. 6287806
; GENERAL INFORMATION:
; APPLICANT: KURIYAMA, Masato
; APPLICANT: KURIYAMA, Masato
; APPLICANT: KOYAMA, No. 6287806uyuki
; APPLICANT: FUKUDA, Tsunehiko
; TITLE OF INVENTION: METHOD FOR PRODUCING A BIOLOGICALLY
; TITLE OF INVENTION: ACTIVE RECOMBINANT CYSTEINE-FREE
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 WATER STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/108,661
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/350,709
; FILING DATE: 07-DEC-1994
; APPLICATION NUMBER: 07/838,857
; FILING DATE: 18-FEB-1992
; APPLICATION NUMBER: JP 024841
; FILING DATE: 19-FEB-1991
; APPLICATION NUMBER: JP 0271438
; FILING DATE: 18-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 41614-FWC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: 200291 STRE
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
US-09-108-661-9

Query Match 98.8%; Score 417; DB 3; Length 84;
Best Local Similarity 98.8%; Pred. No. 1.8e-44;
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 VSEIQLMHNGLKHLNSMERVEWLRKKLDQVHNFVALGAPLAPRDAGSQPRKKEDNVLYE 60
Db 2 VSEIQLMHNGLKHLNSMERVEWLRKKLDQVHNFVALGAPLAPRDAGSQPRKKEDNVLYE 61
QY 61 SHEKSLGEAKADNVNLTAKSQ 83
Db 62 SHEKSLGEAKADNVNLTAKSQ 84

RESULT 8

US-10-002-818-1

; Sequence 1, Application US/10002818
; Patent No. 6524788
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas L.
; TITLE OF INVENTION: Methods for Monitoring Therapeutic Suppression of Parathy
; TITLE OF INVENTION: Renal Patients Having Secondary Hyperparathyroidism
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/002,818
; CURRENT FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Microsoft Word 2000 - ASCII format
; SEQ ID NO 1
; LENGTH: 84
; TYPE: PRT
; ORGANISM: human parathyroid hormone peptide fragment
US-10-002-818-1
Query Match 98.8%; Score 417; DB 4; Length 84;
Best Local Similarity 98.8%; Pred. No. 1.8e-44;
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 VSEIQLMHNGLKHLNSMERVEWLRKKLDQVHNFVALGAPLAPRDAGSQPRKKEDNVLYE 60
Db 2 VSEIQLMHNGLKHLNSMERVEWLRKKLDQVHNFVALGAPLAPRDAGSQPRKKEDNVLYE 61
QY 61 SHEKSLGEAKADNVNLTAKSQ 83
Db 62 SHEKSLGEAKADNVNLTAKSQ 84
RESULT 9
PCT-US95-15800-25
; Sequence 25, Application PC/TUS9515800
; GENERAL INFORMATION:
; APPLICANT: Biogenbraska, Inc.
; TITLE OF INVENTION: PRODUCTION OF PEPTIDES USING
; TITLE OF INVENTION: RECOMBINANT FUSION PROTEIN CONSTRICTS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 Norwest Center, 90 S. 7th Street
; CITY: Minneapolis
; STATE: MN
; COUNTRY: U.S.A.
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/15800
; FILING DATE: 07-DEC-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/350,530
; FILING DATE: 07-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.45USWO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/332-5300
; TELEFAX: 612/332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO

ANTI-SENSE: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
PCT-US95-15800-25

Query Match
Best Local Similarity 98.8%; Score 417; DB 5; Length 84;
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNLGKHLNSMERVWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE 60
DB 2 VSEIQLMHNLGKHLNSMERVWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE 61
QY 61 SHEKSLGEANKADVNVLTKAKSQ 83
DB 62 SHEKSLGEANKADVNVLTKAKSQ 84

RESULT 10

US-08-142-551B-1
Sequence 1, Application US/08142551B
Patent No. 5814603
GENERAL INFORMATION:
APPLICANT: Oldenburg, Kevin R.
TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
STATE: Virginia
COUNTRY: US
ZIP: 22313

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142.551B
FILING DATE: 25-OCT-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/077,296
FILING DATE: 14-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/898,219
FILING DATE: 12-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/965,677
FILING DATE: 22-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Swiss, Gerald F.
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 000324-010
TELEPHONE: (415) 854-7400
TELEFAX: (415) 854-8275
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..84
OTHER INFORMATION: /note= "84 amino acid PTH"

US-08-142-551B-1

Query Match
Best Local Similarity 97.6%; Score 412; DB 2; Length 84;
Matches 81; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 97.6%; Pred. No. 7.5e-44;
Matches 81; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNLGKHLNSMERVWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE 60
DB 2 VSEIQLMHNLGKHLNSMERVWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE 61
QY 61 SHEKSLGEANKADVNVLTKAKSQ 83
DB 62 SHEKSLGEANKADVNVLTKAKSQ 84

RESULT 11

US-08-411-726-1
Sequence 1, Application US/08411726
Patent No. 5880093
GENERAL INFORMATION:

APPLICANT: Bagnoli, Franco
TITLE OF INVENTION: Use of Parathormone, Its Biologically
TITLE OF INVENTION: Active Fragments and Correlated Peptides, for the Preparation
TITLE OF INVENTION: Pharmaceutical Compositions Useful for the Treatment of
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenyon & Kenyon
STREET: 1 Broadway
CITY: New York
STATE: NY
COUNTRY: US
ZIP: 10004

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 6.2
SOFTWARE: Wordperfect 6.1 for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/411,726
FILING DATE: 05-APR-1995
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/02755
FILING DATE: 08-OCT-1993
APPLICATION NUMBER: MI-92A002331
FILING DATE: 09-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: PALMESE, Maria Luisa
REGISTRATION NUMBER: 34,402
REFERENCE/DOCKET NUMBER: 2111/1300
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-425-7200
TELEFAX: 212-425-5288
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-411-726-1

Query Match
Best Local Similarity 97.6%; Score 412; DB 2; Length 84;
Matches 81; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNLGKHLNSMERVWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE 60
DB 2 VSEIQLMHNLGKHLNSMERVWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE 61
QY 61 SHEKSLGEANKADVNVLTKAKSQ 83
DB 62 SHEKSLGEANKADVNVLTKAKSQ 84

RESULT 12

US-07-707-114-1
; Sequence 1, Application US/07707114
; Patent No. 5208041
; GENERAL INFORMATION:
; APPLICANT: SINDREY, Dennis R.
; TITLE OF INVENTION: ESSENTIALLY PURE HUMAN PARATHYROID
; HORMONE
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/707.114
; FILING DATE: 19910523
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16777/147 ALLE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: homo sapiens
; IMMEDIATE SOURCE:
; CLONE: hPTH
US-07-707-114-1

Query Match 96.4%; Score 407; DB 1; Length 84;
Best Local Similarity 96.4%; Pred. No. 3.1e-43;
Matches 80; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 VSEIQLMHNLGKHLNSMERVWLKRLQDVHNFVALGAPLAPRDAGSORPKKEDNVLYE 60
DB 2 VSEIQLMHNLGKHLNSMERVWLKRLQDVHNFVALGAPLAPRDAGSORPKKEDNVLYE 61
QY 61 SHEKSLGEANKADVNLTKAKSQ 83
DB 62 SHEKSLGEANKADVNLTKAKSQ 84

RESULT 13
US-07-773-098-2
; Sequence 2, Application US/07773098
; Patent No. 5317010
; GENERAL INFORMATION:
; APPLICANT: PANG, Peter K.T.
; APPLICANT: JIE, Shan
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES AS
; TITLE OF INVENTION: OSTEOPOROTIC CONTROL AGENTS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Armstrong, Nikaldo, Marmelstein, Kubovcik &
; ADDRESSEE: Murray
; STREET: 1725 K Street, N.W., Suite 1000
; CITY: Washington D.C.
; COUNTRY: United States of America

ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/773.098
; FILING DATE: 19911010
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Murray, Robert B.
; REGISTRATION NUMBER: 22,890
; REFERENCE/DOCKET NUMBER: 901930
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 659-2930
; TELEFAX: (202) 887-0357
; TELEX: 440142
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-773-098-2

Query Match 87.2%; Score 368; DB 1; Length 84;
Best Local Similarity 88.0%; Pred. No. 2.1e-38;
Matches 73; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY 1 VSEIQLMHNLGKHLNSMERVWLKRLQDVHNFVALGAPLAPRDAGSORPKKEDNVLYE 60
DB 2 VSEIQLMHNLGKHLNSMERVWLKRLQDVHNFVALGAPLAPRDAGSORPKKEDNVLYE 61
QY 61 SHEKSLGEANKADVNLTKAKSQ 83
DB 62 SHEKSLGEANKADVNLTKAKSQ 84

RESULT 14
US-08-733-446-5
; Sequence 5, Application US/08733446
; Patent No. 5856138
; GENERAL INFORMATION:
; APPLICANT: FUKUDA, Tsunehiko
; TITLE OF INVENTION: HUMAN PARATHYROID HORMONE MUTAINS AND
; TITLE OF INVENTION: PRODUCTION THEREOF
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/733.446
; FILING DATE: 18-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/402.970
; FILING DATE:
; APPLICATION NUMBER: US/07/926.787
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: NEUNER, George W
; REGISTRATION NUMBER: 26964

REFERENCE/DOCKET NUMBER: 42025
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617)523-3400
 TELEFAX: (617)523-6440
 TELEX: 200291 STRE UR
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 84 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: mutation
 LOCATION: 8 Xaa-Leu, Ile, Val, Phe, Tyr, Trp or Met,
 LOCATION: 18 Xaa-Leu, Ile, Val, Phe, Tyr, Trp or Met,
 LOCATION: 34 Xaa-Cys or Phe, 35 Xaa-Cys or Val,
 LOCATION: 37 Xaa-Cys or Leu, 39 Xaa-Cys or Ala,
 LOCATION: 41 Xaa-Cys or Leu, 43 Xaa-Cys or Pro, 44 Xaa-Cys or Arg
 IDENTIFICATION METHOD: E
 US-08-733-446-5

Query Match 86.3%; Score 364; DB 2; Length 84;
 Best Local Similarity 88.0%; Pred. No. 6.7e-38;
 Matches 73; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
 QY 1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE 60
 DB 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE 61
 QY 61 SHEKSLGEANKADVNVLTAKSQ 83
 DB 62 SHEKSLGEADKADVNVLTAKSQ 84

RESULT 15

US-07-773-098-1
 ; Sequence 1, Application US/07773098
 ; Patent No. 5317010
 ; GENERAL INFORMATION:
 ; APPLICANT: PANG, Peter K.T.
 ; APPLICANT: JIE, Shan
 ; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES AS
 ; TITLE OF INVENTION: OSTEOPOROTIC CONTROL AGENTS
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Armstrong, Mikaido, Marmelstein, Kubovcik &
 ; ADDRESSEE: Murray
 ; STREET: 1725 K Street, N.W., Suite 1000
 ; CITY: Washington D.C.
 ; COUNTRY: United States of America
 ; ZIP: 20006
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/773,098
 ; FILING DATE: 19911010
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Murray, Robert B.
 ; REGISTRATION NUMBER: 22,890
 ; REFERENCE/DOCKET NUMBER: 901930
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 659-2930
 ; TELEFAX: (202) 887-0357
 ; TELEX: 440142
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 84 amino acids
 ; TYPE: AMINO ACID
 ; TOPOLOGY: linear

MOLECULE TYPE: protein
 US-07-773-098-1

Query Match 85.1%; Score 359; DB 1; Length 84;
 Best Local Similarity 85.5%; Pred. No. 2.8e-37;
 Matches 71; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
 QY 1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE 60
 DB 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE 61
 QY 61 SHEKSLGEANKADVNVLTAKSQ 83
 DB 62 SHEKSLGEADKADVNVLTAKSQ 84

Search completed: October 9, 2003, 08:15:10
 Job time: 23.0597 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2003, 08:10:52 ; Search time 154.851 Seconds
(without alignments)
86.365 Million cell updates/sec

Title: US-09-928-048A-4
Perfect score: 422
Sequence: 1 VSEIQLMHNLCGLHNSMERV.....KSLGEANKADYNVLTAKSQ 83

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 600653 seqs, 161128416 residues

Total number of hits satisfying chosen parameters: 600653

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database :
- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/1/pubpaa/US05_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
 - 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
 - 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	422	100.0	83	10	US-09-928-047B-1
2	422	100.0	83	12	US-09-928-048A-4
3	422	100.0	84	10	US-09-928-047B-5
4	422	100.0	84	12	US-09-928-048A-3
5	422	100.0	84	15	US-10-215-770-1
6	418	99.1	82	10	US-09-928-047B-2
7	417	98.8	84	9	US-09-169-786-1
8	417	98.8	84	11	US-09-843-221A-10
9	417	98.8	84	11	US-09-898-398-1
10	417	98.8	115	15	US-10-157-031-50
11	407	94.8	78	10	US-09-928-047B-4
12	395	93.6	78	11	US-09-843-221A-12
13	366	86.7	84	15	US-10-215-770-3
14	359	85.1	84	9	US-09-879-257A-49
15	359	85.1	84	15	US-10-215-770-4

355	84.1	84	15	US-10-215-770-2	Sequence 2, Appli
17	74.6	84	11	US-09-843-221A-11	Sequence 11, Appli
18	73.7	84	15	US-10-215-770-5	Sequence 5, Appli
19	67.8	57	10	US-09-928-047B-8	Sequence 8, Appli
20	60.0	51	10	US-09-928-047B-3	Sequence 3, Appli
21	60.0	51	12	US-09-928-048A-5	Sequence 5, Appli
22	58.5	50	10	US-09-928-047B-7	Sequence 7, Appli
23	58.5	50	12	US-09-928-048A-7	Sequence 7, Appli
24	53.1	44	11	US-09-843-221A-13	Sequence 13, Appli
25	45.7	37	11	US-09-843-221A-15	Sequence 15, Appli
26	45.7	38	9	US-09-169-786-4	Sequence 4, Appli
27	45.7	38	11	US-09-843-221A-14	Sequence 14, Appli
28	45.7	38	12	US-10-245-707-1	Sequence 11, Appli
29	44.5	40	15	US-10-014-162-11	Sequence 9, Appli
30	44.3	37	12	US-10-168-185-9	Sequence 3, Appli
31	41.5	34	9	US-09-169-786-3	Sequence 6, Appli
32	41.5	34	10	US-09-928-047B-6	Sequence 16, Appli
33	41.5	34	11	US-09-843-221A-16	Sequence 20, Appli
34	41.5	34	11	US-09-843-221A-20	Sequence 1, Appli
35	41.5	34	11	US-09-843-221A-161	Sequence 5, Appli
36	41.5	34	12	US-09-928-048A-6	Sequence 8, Appli
37	41.5	34	12	US-10-361-928-1	Sequence 15, Appli
38	41.5	34	12	US-10-361-928-2	Sequence 16, Appli
39	41.5	34	12	US-10-361-928-5	Sequence 2, Appli
40	41.5	34	12	US-10-361-928-8	Sequence 5, Appli
41	41.5	34	12	US-10-340-484-15	Sequence 8, Appli
42	41.5	34	12	US-10-340-484-16	Sequence 15, Appli
43	41.5	34	14	US-10-016-403-5	Sequence 16, Appli
44	41.5	34	14	US-10-097-079-1	Sequence 5, Appli
45	41.5	42	12	US-10-325-021-17	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-928-047B-1
; Sequence 1, Application US/09928047B
; Patent No. US20020160945A1
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas
; TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
; TITLE OF INVENTION: ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
; FILE REFERENCE: 53221-20002.00
; CURRENT APPLICATION NUMBER: US/09/928,047B
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/224,446
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-047B-1

Query Match 100.0%; Score 422; DB 10; Length 83;
Best Local Similarity 100.0%; Pred. No. 2,4e-43;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 VSEIQLMHNLCGLHNSMERVWLRRKLLQDVHFNALGAPLAPRDAGSORPKKEDNVLVE 60
Db 1 VSEIQLMHNLCGLHNSMERVWLRRKLLQDVHFNALGAPLAPRDAGSORPKKEDNVLVE 60
Oy 61 SHEKSLGEANKADYNVLTAKSQ 83
Db 61 SHEKSLGEANKADYNVLTAKSQ 83
RESULT 2
US-09-928-048A-4
; Sequence 4, Application US/09928048A
; Publication No. US20030138858A1

```
; GENERAL INFORMATION:
; APPLICANT: Scantibodies Laboratory, Inc.
; APPLICANT: Cantor, Thomas L.
; TITLE OF INVENTION: METHODS AND DEVICES FOR DIRECT
; TITLE OF INVENTION: DETERMINATION OF CYCLASE INHIBITING PARATHYROID HORMONE
; FILE REFERENCE: 53221-20015.00
; CURRENT APPLICATION NUMBER: US/09/928,048A
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-048A-4

Query Match      100.0%; Score 422; DB 12; Length 83;
Best Local Similarity 100.0%; Pred. No. 2.4e-43;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE 60
Db 1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE 60
QY 61 SHEKSLGEANKADVNVLTKAKSQ 83
Db 61 SHEKSLGEANKADVNVLTKAKSQ 83

RESULT 3
US-09-928-047B-5
; Sequence 5, Application US/09928047B
; Patent No. US20020160945A1
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas
; TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
; TITLE OF INVENTION: ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
; FILE REFERENCE: 53221-20002.00
; CURRENT APPLICATION NUMBER: US/09/928,047B
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/224,446
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-047B-5

Query Match      100.0%; Score 422; DB 10; Length 84;
Best Local Similarity 100.0%; Pred. No. 2.4e-43;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE 60
Db 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE 61
QY 61 SHEKSLGEANKADVNVLTKAKSQ 83
Db 62 SHEKSLGEANKADVNVLTKAKSQ 84

RESULT 4
US-09-928-048A-3
; Sequence 3, Application US/09928048A
; Publication No. US20030138658A1
; GENERAL INFORMATION:
; APPLICANT: Scantibodies Laboratory, Inc.
; APPLICANT: Cantor, Thomas L.
; TITLE OF INVENTION: METHODS AND DEVICES FOR DIRECT
; TITLE OF INVENTION: DETERMINATION OF CYCLASE INHIBITING PARATHYROID HORMONE
; FILE REFERENCE: 53221-20015.00
```

```
; CURRENT APPLICATION NUMBER: US/09/928,048A
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-048A-3

Query Match      100.0%; Score 422; DB 12; Length 84;
Best Local Similarity 100.0%; Pred. No. 2.4e-43;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE 60
Db 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE 61
QY 61 SHEKSLGEANKADVNVLTKAKSQ 83
Db 62 SHEKSLGEANKADVNVLTKAKSQ 84

RESULT 5
US-10-215-770-1
; Sequence 1, Application US/10215770
; Publication No. US20030087822A1
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas L.
; TITLE OF INVENTION: PARATHYROID HORMONE ANTAGONISTS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 53221-20002.20
; CURRENT APPLICATION NUMBER: US/10/215,770
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US 60/224,446
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US 60/224,447
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-215-770-1

Query Match      100.0%; Score 422; DB 15; Length 84;
Best Local Similarity 100.0%; Pred. No. 2.4e-43;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE 60
Db 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE 61
QY 61 SHEKSLGEANKADVNVLTKAKSQ 83
Db 62 SHEKSLGEANKADVNVLTKAKSQ 84

RESULT 6
US-09-928-047B-2
; Sequence 2, Application US/09928047B
; Patent No. US20020160945A1
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas
; TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
; TITLE OF INVENTION: ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
; FILE REFERENCE: 53221-20002.00
; CURRENT APPLICATION NUMBER: US/09/928,047B
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/224,446
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
```


Query Match 98.8%; Score 417; DB 15; Length 115;
Best Local Similarity 98.8%; Pred. No. 1.4e-42;
Matches 82; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSEIQMHNLGKHLNSMERVWLKQDVHNFVALGAPLAPRDAGSORPKKEDNVLYE 60
|||||
DB 33 VSEIQMHNLGKHLNSMERVWLKQDVHNFVALGAPLAPRDAGSORPKKEDNVLYE 92
|||||

QY 61 SHEKSLGEANKADVNLTKAKSQ 83
|||||
DB 93 SHEKSLGEANKADVNLTKAKSQ 115
|||||

RESULT 11
US-09-928-047B-4
; Sequence 4, Application US/09928047B
; Patent No. US20020160945A1
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas
; TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
; TITLE OF INVENTION: ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
; FILE REFERENCE: 53221-20002.00
; CURRENT APPLICATION NUMBER: US/09/928,047B
; CURRENT FILING DATE: 2001-08-10
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-047B-4

Query Match 94.8%; Score 400; DB 10; Length 78;
Best Local Similarity 100.0%; Pred. No. 1e-40;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 LMHNLGKHLNSMERVWLKQDVHNFVALGAPLAPRDAGSORPKKEDNVLYESHEKS 65
|||||

DB 1 LMHNLGKHLNSMERVWLKQDVHNFVALGAPLAPRDAGSORPKKEDNVLYESHEKS 60
|||||

QY 66 LGANKADVNLTKAKSQ 83
|||||

DB 61 LGANKADVNLTKAKSQ 78
|||||

RESULT 12
US-09-843-221A-12
; Sequence 12, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENIUK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID H
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-12

Query Match 93.6%; Score 395; DB 11; Length 78;
Best Local Similarity 98.7%; Pred. No. 4e-40;
Matches 77; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 LMHNLGKHLNSMERVWLKQDVHNFVALGAPLAPRDAGSORPKKEDNVLYESHEKS 65
|||||

DB 1 LMHNLGKHLNSMERVWLKQDVHNFVALGAPLAPRDAGSORPKKEDNVLYESHEKS 60
|||||

QY 66 LGANKADVNLTKAKSQ 83
|||||

DB 61 LGANKADVNLTKAKSQ 78
|||||

RESULT 13
US-10-215-770-3
; Sequence 3, Application US/10215770
; Publication No. US20030087822A1
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas L.
; TITLE OF INVENTION: PARATHYROID HORMONE ANTAGONISTS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 53221-20002.20
; CURRENT APPLICATION NUMBER: US/10/215,770
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US 60/224,446
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US 60/224,447
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Dog
US-10-215-770-3

Query Match 86.7%; Score 366; DB 15; Length 84;
Best Local Similarity 86.7%; Pred. No. 1.4e-36;
Matches 72; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 VSEIQMHNLGKHLNSMERVWLKQDVHNFVALGAPLAPRDAGSORPKKEDNVLYE 60
|||||

DB 2 VSEIQMHNLGKHLNSMERVWLKQDVHNFVALGAPLAPRDAGSORPKKEDNVLYE 61
|||||

QY 61 SHEKSLGEANKADVNLTKAKSQ 83
|||||

DB 62 STQKSLGEANKADVNLTKAKSQ 84
|||||

RESULT 14
US-09-879-257A-49
; Sequence 49, Application US/09879257A
; Patent No. US20020081690A1
; GENERAL INFORMATION:
; APPLICANT: YAMAMOTO, SACHIKO
; APPLICANT: HANADA, TOSHIRO
; APPLICANT: SHIRO, MINORU
; APPLICANT: KOBATAKE, SHINZO
; TITLE OF INVENTION: HYBRID ENZYMES AND USE THEREOF
; FILE REFERENCE: 55986(70281)
; CURRENT APPLICATION NUMBER: US/09/879,257A
; CURRENT FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-879-257A-49

Query Match 85.1%; Score 359; DB 9; Length 84;
Best Local Similarity 85.5%; Pred. No. 9.5e-36;

	Matches	71;	Conservative	5;	Mismatches	7;	Indels	0;	Gaps	0;
QY	1	VSEIQLMNLGKHLNSMERVWLRKQLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE	60							
Db	2	VSEIQLMNLGKHLNSMERVWLRKQLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE	61							
QY	61	SHEKSLGEANKADVNLTKAKSQ	83							
Db	62	SHOKSLGEANKADVNLTKAKSQ	84							

RESULT 15

```

US-10-215-770-4
; Sequence 4, Application US/10215770
; Publication No. US20030087822A1
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas L.
; TITLE OF INVENTION: PARATHYROID HORMONE ANTAGONISTS AND USES
; FILE REFERENCE: 53221-20002.20
; CURRENT APPLICATION NUMBER: US/10/215,770
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US 60/224,446
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US 60/224,447
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Bovine
US-10-215-770-4

```

Query Match	85.1%	Score	359;	DB	15;	Length	84;
Best Local Similarity	85.5%	Pred. No.	9.5e-36;				
Matches	71;	Conservative	5;	Mismatches	7;	Indels	0;
QY	1	VSEIQLMNLGKHLNSMERVWLRKQLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE	60				
Db	2	VSEIQLMNLGKHLNSMERVWLRKQLQDVHNFVALGAPLAPRDAGSORPRKKEDNVLVE	61				
QY	61	SHEKSLGEANKADVNLTKAKSQ	83				
Db	62	SHOKSLGEANKADVNLTKAKSQ	84				

Search completed: October 9, 2003, 08:19:28
Job time : 155.851 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2003, 08:08:56 ; Search time 36.5373 Seconds
(without alignments)
221.556 Million cell updates/sec

Title: US-09-928-048A-5
Perfect score: 253
Sequence: 1 FVALGAPLAPRDAGSORPRK.....KSLGEANKADVNLTKAKSQ 51

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- A_Geneseq_19Jun03.*
- 1: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
 - 2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
 - 3: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
 - 4: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
 - 5: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
 - 6: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
 - 7: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
 - 8: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
 - 9: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
 - 10: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
 - 11: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
 - 12: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
 - 13: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
 - 14: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
 - 15: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
 - 16: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
 - 17: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
 - 18: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
 - 19: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
 - 20: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
 - 21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
 - 22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
 - 23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
 - 24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	253	100.0	51	21	AAB07466
2	253	100.0	51	24	ABG74232
3	253	100.0	57	24	ABG74237
4	253	100.0	78	24	ABG74233
5	253	100.0	82	21	AAB07465
6	253	100.0	82	24	ABG74231
7	253	100.0	83	24	ABG74230
8	253	100.0	84	21	AAB07464
9	253	100.0	84	24	ABG74234

10	248	98.0	51	18	AAW08107	Human parathyroid PTH-(29-84). Synt
11	248	98.0	55	12	AAR11732	hPTH mutein lackin
12	248	98.0	78	14	AAR30852	Leu8 hPTH (7-84) m
13	248	98.0	78	14	AAR30859	Human parathyroid
14	248	98.0	78	23	AAE23725	Parathyroid hormon
15	248	98.0	78	23	AAU73024	hPTH mutein lackin
16	248	98.0	79	14	AAR30853	hPTH mutein lackin
17	248	98.0	80	14	AAR35232	Parathyroid hormon
18	248	98.0	81	14	AAR30854	Human PTH encoded
19	248	98.0	84	13	AAR23790	Oxidation resistan
20	248	98.0	84	13	AAE25571	Oxidation resistan
21	248	98.0	84	13	AAR28845	Oxidation resistan
22	248	98.0	84	13	AAR28846	Oxidation resistan
23	248	98.0	84	13	AAR28847	Oxidation resistan
24	248	98.0	84	13	AAR28848	Oxidation resistan
25	248	98.0	84	13	AAR29561	Oxidation resistan
26	248	98.0	84	13	AAR29562	Oxidation resistan
27	248	98.0	84	13	AAR29563	Oxidation resistan
28	248	98.0	84	13	AAR29564	Oxidation resistan
29	248	98.0	84	13	AAR29565	Oxidation resistan
30	248	98.0	84	13	AAR29566	Oxidation resistan
31	248	98.0	84	13	AAR29567	Oxidation resistan
32	248	98.0	84	13	AAR29568	Oxidation resistan
33	248	98.0	84	14	AAR30860	Leu8 18 hPTH mute
34	248	98.0	84	14	AAR30857	Leu8 hPTH mutein.
35	248	98.0	84	14	AAR42067	Human parathyroid
36	248	98.0	84	14	AAR42068	Stability-enhanced
37	248	98.0	84	14	AAR42069	Stability-enhanced
38	248	98.0	84	14	AAR42070	Stability-enhanced
39	248	98.0	84	14	AAR42071	Stability-enhanced
40	248	98.0	84	14	AAR42072	Stability-enhanced
41	248	98.0	84	14	AAR42073	Stability-enhanced
42	248	98.0	84	14	AAR42074	Stability-enhanced
43	248	98.0	84	14	AAR42075	Stability-enhanced
44	248	98.0	84	14	AAR42076	Stability-enhanced
45	248	98.0	84	14	AAR42077	Stability-enhanced

ALIGNMENTS

RESULT 1
AAB07466
ID AAB07466 standard; protein; 51 AA.
AC AAB07466;
XX
XX 20-OCT-2000 (first entry)
DT
DE Amino acid sequence of human parathyroid hormone antagonist.
XX
KW Human; parathyroid hormone; PTH; hyperparathyroidism; bone disease.
XX
OS Homo sapiens.
XX
PN WO200042437-A1.
XX
PD 20-JUL-2000.
XX
PF 13-JAN-2000; 2000WO-US00855.
XX
PR 14-JAN-1999; 99US-0231422.
PR 26-JUN-1999; 99US-0344639.
XX
XX (SCAN-) SCANTIBODIES LAB INC.
PA
XX
XX WPI; 2000-476147/41.
XX
PT Differentiating between normal parathyroid function and hyperparathyroidism comprises determining and comparing whole parathyroid hormone, parathyroid hormone inhibitory peptide fragment and/or total parathyroid hormone levels -

Disclosure: Page 43; 46pp; English.

The present sequence represents a fragment of human parathyroid hormone (PTH), comprising residues 34-84, which functions as a PTH antagonist. The specification describes a method for differentiating between a person having substantially normal parathyroid function and having hyperparathyroidism. The method comprises determining and comparing at least two of the following parameters: whole parathyroid hormone level, parathyroid hormone inhibitory peptide fragment level and total parathyroid hormone level. The method is used for monitoring (treatments of) parathyroid related bone disease and the effects of therapeutic treatment for hyperparathyroidism.

Sequence 51 AA;

Query Match 100.0%; Score 253; DB 21; Length 51;
Best Local Similarity 100.0%; Pred. No. 9.5e-27;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSQRPKRKEDNVLSHEKSLGEANKADNVNLTAKSQ 51
DB 1 FVALGAPLAPRDAGSQRPKRKEDNVLSHEKSLGEANKADNVNLTAKSQ 51

RESULT 2
ABG74232
ID ABG74232 standard; peptide; 51 AA.
AC ABG74232;

16-APR-2003 (first entry)

Human parathyroid hormone-based CIP, PTH3-84.

Parathyroid hormone; PTH; cyclase activating parathyroid hormone; CAP; cyclase inhibiting parathyroid hormone; CIP; osteoporosis; hypercalcaemia; osteosarcoma; extracellular calcium; PTH3-84.

Homo sapiens.
US2002160945-A1.

31-OCT-2002.

10-AUG-2001; 2001US-0928047.

10-AUG-2000; 2000US-224446P.

(CANT//) CANTOR T L.

Cantor TL;

WPI; 2003-209227/20.

Treating a patient having osteoporosis and is being administered cyclase activating parathyroid hormone or its analogue comprises administering a cyclase inhibiting parathyroid hormone peptide -

Claim 2; Page 3-4; 8pp; English.

The invention relates to treating a patient having osteoporosis comprising administering a cyclase inhibiting parathyroid hormone peptide (CIP) or its conservatively substituted variant exhibiting a parathyroid hormone (PTH) which regulates extracellular calcium levels) antagonist activity to reduce the occurrence of hypercalcaemia or osteosarcoma in the patient resulting from the administration of CAP. The peptide comprises PTH2-84, PTH3-84 and PTH28-84 (appearing as ABG74230 -ABG74233). The present sequence is the CIP PTH3-84.

Sequence 51 AA;

Query Match 100.0%; Score 253; DB 24; Length 51;
Best Local Similarity 100.0%; Pred. No. 9.5e-27;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSQRPKRKEDNVLSHEKSLGEANKADNVNLTAKSQ 51
DB 1 FVALGAPLAPRDAGSQRPKRKEDNVLSHEKSLGEANKADNVNLTAKSQ 51

RESULT 3

ABG74237
ID ABG74237 standard; peptide; 57 AA.

AC ABG74237;

16-APR-2003 (first entry)

Human parathyroid hormone-based CIP, PTH28-84 #2.

Parathyroid hormone; PTH; cyclase activating parathyroid hormone; CAP; cyclase inhibiting parathyroid hormone; CIP; osteoporosis; hypercalcaemia; osteosarcoma; extracellular calcium; PTH28-84.

Homo sapiens.

US2002160945-A1.

31-OCT-2002.

10-AUG-2001; 2001US-0928047.

10-AUG-2000; 2000US-224446P.

(CANT//) CANTOR T L.

Cantor TL;

WPI; 2003-209227/20.

Treating a patient having osteoporosis and is being administered cyclase activating parathyroid hormone or its analogue comprises administering a cyclase inhibiting parathyroid hormone peptide -

Disclosure; Page 5; 8pp; English.

The invention relates to treating a patient having osteoporosis comprising administering a cyclase inhibiting parathyroid hormone peptide (CIP) or its conservatively substituted variant exhibiting a parathyroid hormone (PTH) which regulates extracellular calcium levels) antagonist activity to reduce the occurrence of hypercalcaemia or osteosarcoma in the patient resulting from the administration of CAP. The peptide comprises PTH2-84, PTH3-84 and PTH28-84 (appearing as ABG74230 -ABG74233). The present sequence is the CIP PTH28-84.
Note: This peptide (SEQ ID 8) is included in the sequence listing but is not referred to anywhere else in the specification. However it does represents PTH amino acids 28-84 (unlike ABG74233 which is referred to as PTH28-84 but is actually PTH7-84 and is claimed as being PTH28-34) It is therefore unclear whether the present peptide or the peptide appearing as ABG74233 is actually intended to be claimed.

Sequence 57 AA;

Query Match 100.0%; Score 253; DB 24; Length 57;
Best Local Similarity 100.0%; Pred. No. 1.1e-26;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSQRPKRKEDNVLSHEKSLGEANKADNVNLTAKSQ 51
DB 7 FVALGAPLAPRDAGSQRPKRKEDNVLSHEKSLGEANKADNVNLTAKSQ 57

RESULT 4

ABG74233
ID ABG74233 standard; peptide; 78 AA.

XX

AC ABG74233;
 XX
 DT 16-APR-2003 (first entry)
 XX
 DE Human parathyroid hormone-based CIP, PTH28-84 #1.
 XX
 KW Parathyroid hormone; PTH; cyclase activating parathyroid hormone;
 XX CAP; cyclase inhibiting parathyroid hormone; CIP; osteoporosis;
 KW hypercalcaemia; osteosarcoma; extracellular calcium; PTH28-84.
 XX
 OS Homo sapiens.
 XX
 XX US2002160945-A1.
 PN
 PD 31-OCT-2002.
 XX
 XX 10-AUG-2001; 2001US-0928047.
 PF
 PR 10-AUG-2000; 2000US-224446P.
 XX
 XX (CANT/) CANTOR T L.
 PA
 PI Cantor TL;
 XX
 DR WPI; 2003-209227/20.
 XX
 XX Treating a patient having osteoporosis and is being administered
 PT cyclase activating parathyroid hormone or its analogue comprises
 PT administering a cyclase inhibiting parathyroid hormone peptide -
 XX
 PS Claim 2; Page 4; 8pp; English.
 XX
 CC The invention relates to treating a patient having osteoporosis
 CC comprising administering a cyclase inhibiting parathyroid hormone peptide
 CC (CIP) or its conservatively substituted variant exhibiting a parathyroid
 CC hormone (PTH, which regulates extracellular calcium levels) antagonist
 CC activity to reduce the occurrence of hypercalcaemia or osteosarcoma in
 CC the patient resulting from the administration of CAP. The peptide
 CC comprises PTH2-84, PTH34-84, PTH3-84 and PTH28-84 (appearing as
 CC -ABG74233). The present sequence is the CIP PTH28-84.
 CC Note: This peptide is referred to in the specification as PTH28-34
 CC but actually represents amino acids 7-84 of PTH. It is therefore unclear
 CC whether this peptide (SEQ ID 4) or the peptide appearing as ABG74237
 CC (which does represent amino acids 28-84 of PTH) is actually intended to
 CC be claimed.
 XX
 XX Sequence 78 AA;
 SQ
 Query Match 100.0%; Score 253; DB 24; Length 78;
 Best Local Similarity 100.0%; Pred. No. 1.6e-26;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 FVALGAPLAPRDAGSORPRKEDNVLSHEKSLGEANKADVNVLTAKSQ 51
 DB 28 FVALGAPLAPRDAGSORPRKEDNVLSHEKSLGEANKADVNVLTAKSQ 78
 RESULT 5
 AAB07465
 ID AAB07465 standard; protein; 82 AA.
 XX
 AC AAB07465;
 XX
 XX 20-OCT-2000 (first entry)
 DT
 XX Amino acid sequence of human parathyroid hormone antagonist.
 DE
 XX Human; parathyroid hormone; PTH; hyperparathyroidism; bone disease.
 KW
 XX Homo sapiens.
 OS
 XX WO2000042437-A1.
 PN
 XX

PD 20-JUL-2000.
 XX
 PF 13-JAN-2000; 2000WO-US00855.
 XX
 PR 14-JAN-1999; 99US-0231422.
 PR 26-JUN-1999; 99US-0344639.
 XX
 PA (SCAN-) SCANTIBODIES LAB INC.
 XX
 DR WPI; 2000-476147/41.
 XX
 XX Differentiating between normal parathyroid function and
 PT hyperparathyroidism comprises determining and comparing whole
 PT parathyroid hormone, parathyroid hormone inhibitory peptide fragment
 PT and/or total parathyroid hormone levels -
 XX
 XX Disclosure; Page 42-43; 46pp; English.
 XX
 CC The present sequence represents a fragment of human parathyroid
 CC hormone (PTH), comprising residues 3-84, which functions as a PTH
 CC antagonist. The specification describes a method for differentiating
 CC between a person having substantially normal parathyroid function
 CC and having hyperparathyroidism. The method comprises determining and
 CC comparing at least two of the following parameters: whole parathyroid
 CC hormone level, parathyroid hormone inhibitory peptide fragment level
 CC and total parathyroid hormone level. The method is used for monitoring
 CC (treatments of) parathyroid related bone disease and the effects of
 CC therapeutic treatment for hyperparathyroidism.
 XX
 XX Sequence 82 AA;
 SQ
 Query Match 100.0%; Score 253; DB 21; Length 82;
 Best Local Similarity 100.0%; Pred. No. 1.7e-26;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 FVALGAPLAPRDAGSORPRKEDNVLSHEKSLGEANKADVNVLTAKSQ 51
 DB 32 FVALGAPLAPRDAGSORPRKEDNVLSHEKSLGEANKADVNVLTAKSQ 82
 RESULT 6
 ABG74231
 ID ABG74231 standard; peptide; 82 AA.
 XX
 AC ABG74231;
 XX
 DT 16-APR-2003 (first entry)
 XX
 DE Human parathyroid hormone-based CIP, PTH34-84.
 XX
 KW Parathyroid hormone; PTH; cyclase activating parathyroid hormone;
 KW CAP; cyclase inhibiting parathyroid hormone; CIP; osteoporosis;
 XX hypercalcaemia; osteosarcoma; extracellular calcium; PTH34-84.
 OS
 XX Homo sapiens.
 PN
 XX US2002160945-A1.
 PD 31-OCT-2002.
 XX
 XX 10-AUG-2001; 2001US-0928047.
 PF
 PR 10-AUG-2000; 2000US-224446P.
 XX
 XX (CANT/) CANTOR T L.
 PA
 PI Cantor TL;
 XX
 DR WPI; 2003-209227/20.
 XX
 XX Treating a patient having osteoporosis and is being administered
 PT cyclase activating parathyroid hormone or its analogue comprises
 PT administering a cyclase inhibiting parathyroid hormone peptide -
 XX

KW CAP; cyclase inhibiting parathyroid hormone; CIP; osteoporosis;
 KW hypercalcaemia; osteosarcoma; extracellular calcium.
 OS Homo sapiens.
 XX US2002160945-A1.
 PN 31-OCT-2002.
 XX 10-AUG-2001; 2001US-0928047.
 PF 10-AUG-2000; 2000US-224446P.
 PR (CANTOR) CANTOR T L.
 XX Cantor TL;
 PI WPI; 2003-209227/20.
 XX
 DR Treating a patient having osteoporosis and its being administered
 PT cyclase activating parathyroid hormone or its analogue comprises
 PT administering a cyclase inhibiting parathyroid hormone peptide -
 XX
 PS Disclosure; Fig 1; 8pp; English.
 XX
 CC The invention relates to treating a patient having osteoporosis
 CC comprising administering a cyclase inhibiting parathyroid hormone peptide
 CC (CIP) or its conservatively substituted variant exhibiting a parathyroid
 CC hormone (PTH, which regulates extracellular calcium levels) antagonist
 CC activity to reduce the occurrence of hypercalcaemia or osteosarcoma in
 CC the patient resulting from the administration of CAP. The peptide
 CC comprises PTH2-84, PTH34-84, PTH3-84 and PTH28-84 (appearing as ABG74230
 CC -ABG74233). The present sequence is full length human PTH, the sequence
 CC upon which the CIP peptides are based.
 XX
 SQ Sequence 84 AA;
 Query Match 100.0%; Score 253; DB 24; Length 84;
 Best Local Similarity 100.0%; Pred. No. 1.8e-26;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 FVALGAPLAPRDAGSQRPKRKEDNVLVESHEKSLGEANKADYVNLTKAKSQ 51
 Db 34 FVALGAPLAPRDAGSQRPKRKEDNVLVESHEKSLGEANKADYVNLTKAKSQ 84
 RESULT 10
 AAW08107
 ID AAW08107 standard; peptide; 51 AA.
 XX
 AC AAW08107;
 XX 10-OCT-1997 (first entry)
 DT Human parathyroid hormone residues 34-84.
 XX
 DE Human; parathyroid hormone; PTH; CAMP-producing activity;
 KW bone formation; osteoporosis; hypoparathyroidism; hypertension;
 KW climacteric disturbance.
 XX
 OS Synthetic.
 XX EP748817-A2.
 PN 18-DEC-1996.
 PD 13-JUN-1996; 96EP-0109475.
 XX 15-JUN-1995; 95JP-0148652.
 PR (TAKE) TAKEDA CHEM IND LTD.
 XX
 PA Fukuda T, Habashita J, Nakagawa S, Taketomi S;
 PI

XX WPI; 1997-036114/04.
 DR New parathyroid hormone derivs. - useful in treatment of bone
 XX diseases, hypoparathyroidism and hypertension
 PT Claim 3; Page 39; 42pp; English.
 XX
 CC The sequences given in AAW08103-07 represent fragments of human para-
 CC thyroid hormone (PTH) which were used as Xaa34 in the generic sequence
 CC given in AAW08102. Peptides based on the generic sequence are human PTH
 CC (1-34) derivative peptides. They have potent CAMP-producing activity and
 CC bone formation activity. They may be used in treatment of bone
 CC diseases including osteoporosis, hypoparathyroidism, hypertension
 CC and climacteric disturbance. The peptides are low in toxicity and
 CC are safe.
 XX
 SQ Sequence 51 AA;
 Query Match 98.0%; Score 248; DB 18; Length 51;
 Best Local Similarity 98.0%; Pred. No. 4.5e-26;
 Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 FVALGAPLAPRDAGSQRPKRKEDNVLVESHEKSLGEANKADYVNLTKAKSQ 51
 Db 1 FVALGAPLAPRDAGSQRPKRKEDNVLVESHEKSLGEANKADYVNLTKAKSQ 51
 RESULT 11
 AAR11732
 ID AAR11732 standard; Protein; 55 AA.
 XX
 AC AAR11732;
 XX 25-MAR-2003 (updated)
 DT 03-JUL-1991 (first entry)
 XX
 DE PTH-(29-84).
 XX
 KW Parathyroid hormone; calcium; osteoporosis; bone.
 XX
 OS Synthetic.
 XX WO9105050-A.
 PN 18-APR-1991.
 PD 01-OCT-1990; 90WO-C000335.
 PF 29-SEP-1989; 89CA-0615001.
 PR (CANA) NAT RES COUNCIL CANADA.
 XX
 PA Sung WL;
 PI WPI; 1991-132857/18.
 DR N-PSDB; AAQ11618.
 XX
 PT Mature human parathyroid synthesis - includes using eg E. coli
 PT transformed by plasmid contg. synthetic nucleotide sequence contg.
 PT adenine rich codons in N-terminal region.
 XX
 PS Disclosure; Fig 6; 62pp; English.
 XX
 CC Codons 29-84 are degenerate in the usage frequency favoured by
 CC E.coli or yeast. Codons 1-28 (see AAQ11617) are designed to contain
 CC adenine rich codons. The sequence is prepd. from eight oligo-
 CC nucleotides (4 on each strand). A plasmid contg. the complete
 CC sequence expresses PTH with an improved yield. PTH is a blood
 CC calcium regulator known to increase bone mass.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX

SQ Sequence 55 AA;
 Query Match 98.0%; Score 248; DB 12; Length 55;
 Best Local Similarity 98.0%; Pred. No. 5e-26;
 Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FVALGAPLAPRDAGSORPRKKEDNVLSHESKSLGEADKADNVNLTAKSQ 51
 DB 5 FVALGAPLAPRDAGSORPRKKEDNVLSHESKSLGEADKADNVNLTAKSQ 55
 RESULT 12
 AAR30852
 ID AAR30852 standard; Protein; 78 AA.
 XX AAR30852;
 AC
 XX
 DT 25-MAR-2003 (updated)
 DT 09-JUN-1993 (first entry)
 XX
 DE hPTH mutein lacking 6 N-terminal amino acids.
 XX
 XX Human parathyroid hormone; hPTH; antagonist; hypoparathyroidism;
 KW hypercalcaemia.
 XX
 OS Synthetic.
 XX
 XX EP528271-A1.
 XX
 XX 24-FEB-1993.
 XX
 XX 05-AUG-1992; 92EP-0113322.
 PF
 XX 07-AUG-1991; 91JP-0198056.
 PR 26-JUN-1992; 92JP-0169713.
 XX
 XX (TAKE) TAKEDA CHEM IND LTD.
 PA
 XX Fukuda T;
 PI
 XX WPI; 1993-060187/08.
 DR N-PSDB; AAQ35228.
 XX
 XX New human parathyroid mutein(s) - useful for treating e.g.
 PT osteoporosis, hypoparathyroidism, hyperparathyroidism,
 PT hypercalcaemia, hypertension etc.
 XX
 PS Disclosure; Page 7; 88pp; English.
 XX
 CC The sequence is that of a human parathyroid hormone (hPTH) peptide
 CC lacking 6 hPTH N-terminal amino acids. The peptide can have higher
 CC stability, enhanced activity and improved absorption by tissues.
 CC It can act as a PTH antagonist and can be used as a therapeutic
 CC agent for hypercalcaemia and hyperparathyroidism.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 78 AA;
 Query Match 98.0%; Score 248; DB 14; Length 78;
 Best Local Similarity 98.0%; Pred. No. 7.6e-26;
 Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FVALGAPLAPRDAGSORPRKKEDNVLSHESKSLGEADKADNVNLTAKSQ 51
 DB 28 FVALGAPLAPRDAGSORPRKKEDNVLSHESKSLGEADKADNVNLTAKSQ 78
 RESULT 13
 AAR30859
 ID AAR30859 standard; Protein; 78 AA.
 XX AAR30859;
 AC
 XX

DT 25-MAR-2003 (updated)
 DT 09-JUN-1993 (first entry)
 XX
 DE Leu8 hPTH (7-84) mutein.
 XX
 KW Human parathyroid hormone; hPTH; antagonist; hypoparathyroidism;
 KW hypercalcaemia.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Region 2
 FT /note= "Met -> Leu"
 XX
 XX EP528271-A1.
 XX
 XX 24-FEB-1993.
 PD
 XX 05-AUG-1992; 92EP-0113322.
 PF
 XX 07-AUG-1991; 91JP-0198056.
 PR 26-JUN-1992; 92JP-0169713.
 XX
 XX (TAKE) TAKEDA CHEM IND LTD.
 PA
 XX Fukuda T;
 PI
 XX WPI; 1993-060187/08.
 DR N-PSDB; AAQ36836.
 XX
 XX New human parathyroid mutein(s) - useful for treating e.g.
 PT osteoporosis, hypoparathyroidism, hyperparathyroidism,
 PT hypercalcaemia, hypertension etc.
 XX
 PS Example; Page 22; 88pp; English.
 XX
 CC The sequence is that of mutated human parathyroid hormone (hPTH)
 CC (7-84) where Met8 is substd. by Leu. It has higher stability, enhanced
 CC activity and improved absorption by tissues. It can act as a PTH
 CC antagonist and can be used as a therapeutic agent for hypercalcaemia
 CC and hyperparathyroidism.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 78 AA;
 Query Match 98.0%; Score 248; DB 14; Length 78;
 Best Local Similarity 98.0%; Pred. No. 7.6e-26;
 Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FVALGAPLAPRDAGSORPRKKEDNVLSHESKSLGEADKADNVNLTAKSQ 51
 DB 28 FVALGAPLAPRDAGSORPRKKEDNVLSHESKSLGEADKADNVNLTAKSQ 78
 RESULT 14
 AAE23725
 ID AAE23725 standard; peptide; 78 AA.
 XX
 AC AAE23725;
 XX
 DT 10-SEP-2002 (first entry)
 XX
 XX Human parathyroid hormone (hPTH) peptide (7-84).
 DE
 XX Human parathyroid hormone; hPTH; PTH-related peptide; PTHrP; eczema;
 KW hyperproliferative skin disorder; psoriasis; ichthyosis; skin cancer;
 KW acne; actinic keratosis; alopecia; gene therapy.
 XX
 OS Homo sapiens.
 XX
 XX WO200228420-A2.
 PN
 XX 11-APR-2002.
 PD

XX PF 05-OCT-2001; 2001WO-US31082.
 XX PR 06-OCT-2000; 2000US-238134P.
 XX PA (HOLICK) HOLICK M F.
 XX PI Hollick MF;
 XX PI WPI: 2002-452304/48.
 DR N-PSDB; AAD37995.
 DR XX
 DR XX
 DR XX
 PT Regulating mammalian skin or hair cell proliferation and
 PT differentiation by administering nucleic acids encoding peptides
 PT derived from N-terminal region of human parathyroid hormone (hPTH) or
 PT hPTH-related protein
 XX
 XX Claim 35; Fig 15; 56pp; English.
 CC The invention relates to a method for regulating proliferation or
 CC enhancing differentiation of mammalian skin or hair cell. The method
 CC involves administering nucleic acids encoding peptides derived from
 CC N-terminal region of human parathyroid hormone (hPTH) or hPTH-related
 CC peptide (PTHrP). The method is used for inhibiting hyperproliferative
 CC skin disorders such as psoriasis, ichthyosis, eczema, acne, actinic
 CC keratosis, skin cancer, for inhibiting hair growth or preventing hair
 CC regrowth. It is useful for stimulating cell growth, rejuvenating aged
 CC skin, preventing skin wrinkles, treating skin wrinkles, enhancing wound
 CC healing, stimulating hair growth, maintaining hair growth, treating or
 CC preventing female or male pattern baldness, for treating chemotherapy
 CC induced alopecia and also for stimulating epidermal cell growth or
 CC hair follicle cell growth. The method is also used in gene therapy.
 CC The present sequence is hPTH peptide.
 XX
 XX Sequence 78 AA;
 SQ
 Query Match 98.0%; Score 248; DB 23; Length 78;
 Best Local Similarity 98.0%; Pred. No. 7.6e-26;
 Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FVALGAPLAPRDAGSORPRKKEDNVLVESHSKSLGAEADKADYNVLTAKSQ 51
 Db 28 FVALGAPLAPRDAGSORPRKKEDNVLVESHSKSLGAEADKADYNVLTAKSQ 78
 RESULT 15
 AAU73024
 ID AAU73024 standard; Peptide; 78 AA.
 AC AAU73024;
 XX
 XX 12-MAR-2002 (first entry)
 XX
 DE Parathyroid hormone PTH/PTHrP modulating domain #6.
 KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;
 KW PTHrP; bone resorption inhibitor; osteoprotegerin; OPG; OPG-L antibody;
 KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;
 KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;
 KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
 KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;
 KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
 KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
 KW immunoglobulin G; IgG.
 OS Homo sapiens.
 XX
 XX WO200181415-A2.
 XX
 XX 01-NOV-2001.
 XX
 XX 27-APR-2001; 2001WO-US13528.

PR 27-APR-2000; 2000US-200053P.
 PR 28-JUN-2000; 2000US-214860P.
 PR 06-FEB-2001; 2001US-266673P.
 PR 26-APR-2001; 2001US-0843221.
 XX
 XX (ANGE-) AMGEN INC.
 PA
 PI Kostenuik P, Liu C, Lacey DL;
 XX
 XX WPI: 2002-066435/09..
 DR
 DR
 PT Composition; useful for treating osteopenia, comprises parathyroid
 PT hormone and parathyroid hormone-related protein receptor modulators
 XX
 PS Disclosure; Page 26; 107pp; English.
 XX
 XX The invention relates to a composition (I) comprising modulators of
 CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
 CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
 CC as osteoprotegerin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
 CC oestrogens, oestrogen receptor modulators and tibolone is useful for
 CC treating osteopenia. (I) is useful for therapeutic and prophylactic
 CC purposes. Antagonists of PTH receptor are useful in treating primary and
 CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
 CC particularly breast and prostate cancer, cachexia and anorexia,
 CC osteopenia, including various forms of osteoporosis, Paget's disease of
 CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
 CC traumatic injury or nontraumatic necrosis associated with Gaucher's
 CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
 CC arthritis, periodontal disease and alopecia. PTH receptor agonists are
 CC useful as therapeutic agents in conditions including fracture repair
 CC (including healing of non-union fractures), osteopenia, including various
 CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
 CC and parathyroid hormone related protein (PTH/PTHrP) modulators and
 CC related amino acid sequences of the invention.
 XX
 XX Sequence 78 AA;
 SQ
 Query Match 98.0%; Score 248; DB 23; Length 78;
 Best Local Similarity 98.0%; Pred. No. 7.6e-26;
 Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FVALGAPLAPRDAGSORPRKKEDNVLVESHSKSLGAEADKADYNVLTAKSQ 51
 Db 28 FVALGAPLAPRDAGSORPRKKEDNVLVESHSKSLGAEADKADYNVLTAKSQ 78
 Search completed: October 9, 2003, 08:10:46
 Job time : 38.0373 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2003, 08:08:56 ; Search time 18.2687 Seconds
(without alignments)
268.471 Million cell updates/sec

Title: US-09-928-048a-5
Perfect score: 253
Sequence: 1 FVALGAPLAPRDAGSQRPK.....KSLGANKADNVLTAKSQ 51

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	248	98.0	115	1 PTHU	parathyroid hormon
2	206	81.4	115	2 JC4202	parathyroid hormon
3	199	78.7	115	1 PTPB	parathyroid hormon
4	194	76.7	115	1 PTPG	parathyroid hormon
5	160	63.2	105	2 I51851	parathyroid hormon
6	160	63.2	115	2 A05091	parathyroid hormon
7	68.5	27.1	119	2 A34937	parathyroid hormon
8	65	25.7	283	2 H86803	parathyroid hormon
9	63.5	25.1	487	2 A71407	prophage p13 prote
10	63	24.9	1937	2 I38055	probable Ste20-lik
11	61.5	24.3	366	2 A64028	myosin heavy chain
12	61	24.1	565	2 G89813	hypothetical prote
13	60.5	23.9	555	2 T44010	DNA polymerase III
14	60	23.7	258	2 A02985	virion protein Iim
15	60	23.7	955	2 S24348	myosin heavy chain
16	60	23.7	1938	2 A59293	myosin heavy chain
17	60	23.7	1940	2 A29320	skeletal myosin he
18	60	23.7	1570	2 T15348	myosin heavy chain
19	59.5	23.5	1400	2 T33758	hypothetical prote
20	59	23.3	404	2 C64597	lipopolysaccharide
21	58.5	23.1	142	2 T45922	probable C2H2-type
22	58	22.9	234	2 S33732	myosin alpha heavy
23	58	22.9	465	2 A02986	myosin alpha heavy
24	58	22.9	1038	1 MWRBCB	myosin beta heavy
25	58	22.9	1935	1 S06006	myosin beta heavy
26	58	22.9	1935	1 S06006	myosin beta heavy
27	58	22.9	1935	2 A59286	myosin heavy chain
28	57.5	22.7	378	2 F56653	virion protein - h
29	56.5	22.3	655	2 C71438	hypothetical prote

RESULT 1

PTHU

parathyroid hormone precursor [validated] - human

N:Alternate names: parathyroid hormone

C:Species: Homo sapiens (man)

C>Date: 24-Apr-1984 #sequence_revision 19-Jan-1996 #text_change 08-Dec-2000

C:Accession: A19339; S53790; A93169; S21199; A93789; A93783; A90426; A94

R:Vasicek, T.J.; McDevitt, B.E.; Freeman, M.W.; Fennick, B.J.; Hendy, G.N.; Pott

PROC. Natl. Acad. Sci. U.S.A. 80, 2127-2131, 1983

A>Title: Nucleotide sequence of the human parathyroid hormone gene.

A:Reference number: A19339; MUID:83169834; PMID:6220408

A:Accession: A19339

A:Molecule type: DNA

A:Residues: 1-115 <V>

A:Cross-references: GB:J00301; NID:g190702; PIDN:AAA60215.1; PID:g190704

R:Yamaguchi, T.; Fukase, M.; Sugimoto, T.; Kido, H.; Chihara, K.

Biol. Chem. Hoppe-Seyler 375, 821-824, 1994

A>Title: Purification of meprin from human kidney and its role in parathyroid ho

A:Reference number: S53790; MUID:95225988; PMID:7710697

A:Accession: S53790

A:Molecule type: protein

A:Residues: 'X', 33, 'X', 35-46; 65-84; 105-110 <V>

A:Note: peptides generated in vitro and in vivo by meprin; peptide cleavage also

R:Jacobs, J.W.; Kemper, B.; Niall, H.D.; Habener, J.F.; Potts Jr., J.T.

Nature 249, 155-157, 1974

A>Title: Structural analysis of human parathyroid hormone by a new microsequer

A:Reference number: A93169; MUID:74174967; PMID:4833516

A:Accession: A93169

A:Molecule type: protein

A:Residues: 26-37 <J>

R:Olstad, O.K.; Reppe, S.; Gabrielsen, O.S.; Hartmanis, M.; Blingsmo, O.R.; Gauti

Eur. J. Biochem. 205, 311-319, 1992

A>Title: Isolation and characterization of two biologically active O-glycosylate

ation.

A:Reference number: S21199; MUID:92209518; PMID:1555591

A:Accession: S21199

A:Molecule type: protein

A:Residues: 32-114, 'N' <L>

A:Note: cloned sequence expressed in Saccharomyces cerevisiae exhibited O-glycosyl

R:Niall, H.D.; Sauer, R.T.; Jacobs, J.W.; Keutmann, H.T.; Segre, G.V.; O'Riordan,

Proc. Natl. Acad. Sci. U.S.A. 71, 384-388, 1974

A>Title: The amino-acid sequence of the amino-terminal 37 residues of human parat

A:Reference number: A93789; MUID:74111656; PMID:4521809

A:Accession: A93789

A:Molecule type: protein

A:Residues: 32-68 <NIA>

R:Brewer Jr., H.B.; Fairwell, T.; Ronan, R.; Sizemore, G.W.; Arnaud, C.D.

Proc. Natl. Acad. Sci. U.S.A. 69, 3585-3588, 1972

A>Title: Human parathyroid hormone: amino-acid sequence of the amino-terminal res

A:Reference number: A93783; MUID:73070429; PMID:4509319

A:Accession: A93783

A:Molecule type: protein

ALIGNMENTS

hypothetical prote
hypothetical prote
DNA-damage repair
hypothetical prote
slow myosin heavy
myosin heavy chain
hypothetical prote
DNA-binding protei
hypothetical prote
neurofilament trip
neurofilament trip
disacylglycerol kin
hypothetical prote
synaptonemal compl
probable purine nu
myosin heavy chain

30 56.5 22.3 674 2 B71438
31 56.5 22.3 727 2 T24284
32 56 22.1 396 2 G96934
33 56 22.1 1787 2 G97222
34 56 22.1 1931 2 A59234
35 56 22.1 1938 1 JX0178
36 55.5 21.9 412 2 T51080
37 55.5 21.9 1203 2 S26650
38 55 21.7 269 2 T15500
39 55 21.7 854 2 S02003
40 55 21.7 1072 1 A37221
41 55 21.7 1154 2 T18525
42 55 21.7 1157 2 T19187
43 55 21.7 1505 2 T1418
44 55 21.7 1518 2 S37928
45 55 21.7 1934 2 I48153

A:Residues: 32-52, 'Q', 54-58, 'K', 60, 'L', 62-65 <BRE>
A:Note: this sequence was determined by sequenator and mass spectroscopic identification
R:Keutmann, H.T.; Niall, H.D.; O'Riordan, J.L.H.; Potts Jr., J.T.
Biochemistry 14, 1842-1847, 1975
A:Title: A reinvestigation of the amino-terminal sequence of human parathyroid hormone.
A:Reference number: A90387; MUID:75146516; PMID:1125201
A:Accession: A90387
A:Molecule type: protein
A:Residues: 52-75 <KE3>
R:Keutmann, H.T.; Sauer, M.M.; Hendy, G.N.; O'Riordan, J.L.H.; Potts Jr., J.T.
Biochemistry 17, 5723-5729, 1978
A:Title: Complete amino acid sequence of human parathyroid hormone.
A:Reference number: A90426; MUID:75082855; PMID:728431
A:Accession: A90426
A:Molecule type: protein
A:Residues: 61-106, 'D', 108-115 <KEU>
R:Keutmann, H.T.; Niall, H.D.; Jacobs, J.W.; Barling, P.M.; Hendy, G.N.; O'Riordan, J.L.H.
in Calcium-regulating Hormones, Talmadge, R.V., Owen, M., and Parsons, J.A., eds., pp.9-14
A:Reference number: A94410
A:Accession: A94410
A:Molecule type: protein
A:Residues: 75-100 <KE2>
R:Tregear, G.W.; van Rietschoten, J.; Green, E.; Niall, H.D.; Keutmann, H.T.; Parsons, J.
Hoppe-Seivler's Z. Physiol. Chem. 355, 415-421, 1974
A:Title: Solid-phase synthesis of the biologically active N-terminal 1-34 peptide of human parathyroid hormone.
A:Reference number: A91660; MUID:75059220; PMID:4474131
A:Contents: annotation; synthesis of residues 32-65
A:Note: the biologically active amino-terminal 34 residues of parathyroid hormone were synthesized at renal adenylate cyclase assay and with the bovine hormone's active region in the child
R:Andreatta, R.H.; Hartmann, A.; Joehl, A.; Kamber, B.; Maier, R.; Riniker, B.; Rittel, Hely. Chim. Acta 56, 470-473, 1973
A:Title: Synthese der Sequenz 1-34 von menschlichem Parat-hormon.
A:Reference number: A91635; MUID:73227467; PMID:4721748
A:Contents: annotation; synthesis of residues 32-65
A:Note: the amino-terminal 34 residues of the parathyroid hormone sequence as determined into thyroparathyroidectomized rats caused a distinct increase in plasma calcium level
R:Hendy, G.N.; Kronenberg, H.M.; Potts, J.T.
Proc. Natl. Acad. Sci. U.S.A. 78, 7365-7369, 1981
A:Title: Nucleotide sequence of cloned cDNAs encoding human preproparathyroid hormone.
A:Reference number: I38342; MUID:82150870; PMID:6950381
A:Accession: I38342
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-115 <RES>
A:Cross-references: EMBL:V00597; NID:g37143; PIDN:CAA23843.1; PID:g37144
C:Genetics:
A:Gene: GDB:PTH
A:Cross-references: GDB:119522; OMIM:168450
A:Map position: 11p15.2-11p15.1
A:Introns: 29/2
A:Note: the first intron occurs before the initiator codon
C:Function:
A:Description: factor in homeostatic control of plasma calcium and phosphate; released F counter to calcitonin
C:Superfamily: parathyroid hormone; parathyroid hormone homology
C:Keywords: calcium; hormone; parathyroid gland; plasma
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-31/Domain: propeptide #status experimental <PRO>
F:30-64/Domain: parathyroid hormone homology <PTH>
F:32-115/Product: parathyroid hormone #status experimental <MAT>
Query Match 98.0%; Score 248; DB 1; Length 115;
Best Local Similarity 98.0%; Pred. No. 7e-23;
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
..OY 1 FVALGAPLAPDAGSORPRKKEDNVLVESHEKSLGAEADKADNVNLTAKSQ 51
Db 65 FVALGAPLAPDAGSORPRKKEDNVLVESHEKSLGAEADKADNVNLTAKSQ 115
RESULT 2
JC4202
parathyroid hormone precursor - dog

A:Reference number: A93776; MUID:71091588; PMID:4322265
 A:Contents: annotation; synthesis of residues 32-65
 A>Note: the synthetic peptide was active in vivo and in vitro
 R:Brewer Jr., H.B.; Fairwell, T.; Rittel, W.; Littledike, T.; Arnaud, C.D.
 Am. J. Med. 56, 759-766, 1974
 A:Title: Recent studies on the chemistry of human, bovine and porcine parathyroid hormone
 A:Reference number: A90030; MUID:74173303; PMID:4598526
 A:Contents: annotation
 R:Weaver, C.A.; Gordon, D.F.
 Proc. Natl. Acad. Sci. U.S.A. 78, 4073-4077, 1981
 A:Title: Introduction by molecular cloning of artifactual inverted sequences at the 5' end of the parathyroid hormone gene
 A:Reference number: I45975
 A:Accession: I45975
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-115 <WE2>
 A:Cross-references: GB:J00024; NID:g163642; PIDN:AAA30747.1; PID:g163643
 R:Weaver, C.A.; Gordon, D.F.
 Mol. Cell. Endocrinol. 28, 411-424, 1982
 A:Title: Nucleotide sequence of bovine parathyroid hormone messenger RNA.
 A:Reference number: I45976; MUID:83105964; PMID:6185374
 A:Accession: I45976
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-115 <WE3>
 A:Cross-references: GB:M25082; NID:g163644; PIDN:AAA30748.1; PID:g163645
 C:Genetics: PTH
 A:Gene: PTH
 A:Introns: 29/2
 C:Superfamily: parathyroid hormone; parathyroid hormone homology
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:26-31/Domain: propeptide #status experimental <PRO>
 F:30-64/Domain: parathyroid hormone homology <PTH>
 F:32-115/Domain: parathyroid hormone #status experimental <MAT>
 Query Match 78.7%; Score 199; DB 1; Length 115;
 Best Local Similarity 80.4%; Pred. No. 6e-17;
 Matches 41; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 QY 1 FVALGAPLAPRDAGSORPRKEDNVLSHESKSLGAEKADNVNLTAKSQ 51
 DB 65 FVALGASIVHRDGGSORPRKEDNVLSHESKSLGAEKADNVNLTAKSQ 115
 RESULT 4
 PTPG
 parathyroid hormone precursor - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 24-Apr-1984 #sequence_revision 12-Apr-1996 #text_change 18-Jun-1999
 C:Accession: B26806; A90390; A90376; A01535
 R:Schmelzer, H.J.; Gross, G.; Widera, G.; Mayer, H.
 Nucleic Acids Res. 15, 6740, 1987
 A:Title: Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid hormone
 A:Reference number: A36806; MUID:87316938; PMID:3628009
 A:Accession: B26806
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-115 <SCH>
 A:Cross-references: GB:X05722; GB:X00409; NID:g1838; PIDN:CAA29193.1; PID:g1839
 R:Chu, L.L.H.; Huang, W.Y.; Littledike, E.T.; Hamilton, J.W.; Cohn, D.V.
 Biochemistry 14, 3631-3635, 1975
 A:Title: Porcine parathyroid hormone. Identification, biosynthesis, and partial amino acid sequence
 A:Reference number: A90390; MUID:76018954; PMID:1164500
 A:Accession: A90390
 A:Molecule type: protein
 A:Residues: 26-115 <CHU>
 R:Sauer, R.T.; Niall, H.D.; Hogan, M.L.; Keutmann, H.T.; O'Riordan, J.L.H.; Potts Jr., J.
 Biochemistry 13, 1994-1999, 1974
 A:Title: The amino acid sequence of porcine parathyroid hormone.
 A:Reference number: A90376; MUID:74253317; PMID:4840833
 A:Accession: A90376

A:Molecule type: protein
 A:Residues: 32-109 <SAD>
 R:Brewer Jr., H.B.; Fairwell, T.; Rittel, W.; Littledike, T.; Arnaud, C.D.
 Am. J. Med. 56, 759-766, 1974
 A:Title: Recent studies on the chemistry of human, bovine and porcine parathyroid hormone
 A:Reference number: A90030; MUID:74173303; PMID:4598526
 A:Contents: annotation
 C:Superfamily: parathyroid hormone; parathyroid hormone homology
 F:1-25/Domain: signal sequence #status predicted <SIG>
 F:26-31/Domain: propeptide #status experimental <PRO>
 F:30-64/Domain: parathyroid hormone homology <PTH>
 F:32-115/Domain: parathyroid hormone #status experimental <MAT>
 Query Match 76.7%; Score 194; DB 1; Length 115;
 Best Local Similarity 78.4%; Pred. No. 2.4e-16;
 Matches 40; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
 QY 1 FVALGAPLAPRDAGSORPRKEDNVLSHESKSLGAEKADNVNLTAKSQ 51
 DB 65 FVALGASIVHRDGGSORPRKEDNVLSHESKSLGAEKADNVNLTAKSQ 115
 RESULT 5
 I51851
 parathyroid hormone - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
 C:Accession: I51851
 R:Schmelzer, H.
 Adv. Gene Technol. 21, 228-229, 1984
 A:Title: Nucleotide sequence of cloned cDNA encoding rat prepro parathyroid hormone
 A:Reference number: I51851
 A:Accession: I51851
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-105 <RES>
 A:Cross-references: GB:M54875; NID:g601932; PIDN:AAA57156.1; PID:g601933
 C:Genetics: PTH
 A:Gene: PTH
 C:Superfamily: parathyroid hormone; parathyroid hormone homology
 F:20-54/Domain: parathyroid hormone homology <PTH>
 Query Match 63.2%; Score 160; DB 2; Length 105;
 Best Local Similarity 62.7%; Pred. No. 2.9e-12;
 Matches 32; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
 QY 1 FVALGAPLAPRDAGSORPRKEDNVLSHESKSLGAEKADNVNLTAKSQ 51
 DB 55 FVSLGVQMAARBSYORPTKKEENVLDGNSKSLGEGDKADVDVLKAKSQ 105
 RESULT 6
 A05091
 parathyroid hormone precursor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 16-Jul-1999
 C:Accession: A05091; A26806
 R:Heinrich, G.; Kronenberg, H.M.; Potts Jr., J.T.; Habener, J.F.
 J. Biol. Chem. 259, 3320-3329, 1984
 A:Reference number: A05091; MUID:84135846; PMID:6321505
 A:Accession: A05091
 A:Molecule type: DNA
 A:Residues: 1-115 <HEI>
 A:Cross-references: GB:K01268; NID:g206483; PIDN:AAA41979.1; PID:g206485
 A>Note: the authors translated the codon GAA for residue 87 as Asp
 R:Schmelzer, H.J.; Gross, G.; Widera, G.; Mayer, H.
 Nucleic Acids Res. 15, 6740, 1987
 A:Title: Nucleotide sequence of a full-length cDNA clone encoding preproparathyroid hormone
 A:Reference number: A36806; MUID:87316938; PMID:3628009
 A:Accession: A26806
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA

probable Ste20-like kinase - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
A:Variety: columbia
C:Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 16-Dec-1998

C: Accession: A74307
R: Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Berkamp,
P.; Wedler, H.; Wedler, R.; Weitneggger, T.; Pohl, T.M.; Terryn,
Avanagh, T.; Hempel, S.; Kötter, p.; Entian, K.D.; Rieger, M.; Schaeffer, M.; F.
Nature 391, 485-488, 1998
A: Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Pui-
erhoff, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman
C.; Chwalwaizis, N.

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-487 <BEV>
A:Cross-references: GB:Z97336; NID:G2244788; PID:E326893; PID:G2244804
C:Genetics:
A:Map position: 4COP9-4C3845
C:Superfamily: protein kinase homology
F:13-293/Domain: protein kinase homology <KIN>

RESULT 10
I38055
myosin heavy chain, perinatal skeletal muscle - human
N:Contains: myosin ATPase (EC 3.6.4.1)
C:Species: Homo sapiens (man)

C;Species: Homo sapiens (man)
C;Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 19-Apr-2002
C;Accession: I38055; JH0154; S12459; S09332; A30220; S49478
R;Jullian, E.H.; Kelly, A.M.; Pompidou, A.J.; Hoffman, R.; Schiaffino, S.; Sted
Eur. J. Biochem. 230, 1001-1006, 1995

A>Title: Characterization of a human perinatal myosin heavy-chain transcript.
A:Reference number: I38055; MID:95324556; PMID:7601129
A:Accession: I38055
A>Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: mRNA
A:Residues: 1-1937 <RES>
A:CROSS-references: EMBL:Z38133; NID:G558668; PIDN:CAR86293.1; PID:G558669
R:Karsch-Mizrachi, R.; Peghail, R.; Shows, T.B.; Leinwand, L.A.
Gene 89, 289-294, 1990
A>Title: Generation of a full-length human perinatal myosin heavy-chain-encoding
A:Reference number: JH0154; MID:90323631; PMID:2373371
A:Accession: JH0154
A:Molecule type: mRNA
A:Residues: 1-14, 'A', 16-859 <KAR>
A:CROSS-references: GB:Y00821
A:Experimental source: skeletal muscle
R:Bober, E.
submitted to the EMBL Data Library, January 1989
A:Reference number: S12458
A:Accession: S12459

RESULT 12

myosin heavy chain, skeletal muscle - rabbit (fragment)
C/Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 13-Feb-1998

C/Accession: A02985

R/Capony, J.P.; Elzinga, M.

Biophys. J. 33, 148a, 1981

A:Reference number: A02985

A:Accession: A02985

A:Molecule type: protein

A:Residues: 1-258 <CAP>

A>Note: this fragment is from the heavy meromyosin subfragment-2

C:Superfamily: myosin heavy chain; myosin motor domain homology

C:Keywords: actin binding; ATP; coiled coil; muscle; skeletal muscle

Query Match 23.7%; Score 60; DB 2; Length 258;
Best Local Similarity 42.4%; Pred. No. 9.6;
Matches 14; Conservative 8; Mismatches 9; Indels 2; Gaps 1;

Oy 21 KEDNVLVESHEKSLG--EANKADVNVLTAKSQ 51

|| | | | | | | | | | | | | | | | | | | | |

Db 152 KEKKALQEAHQOTLDDQLQAEEDKVNTLTAKTK 184

RESULT 15

S24348

myosin heavy chain, embryonic and adult skeletal muscle (clone Cemb2) - chicken (fragment)

C:Species: Gallus gallus (chicken)

C>Date: 03-Feb-1994 #sequence_revision 06-Sep-1996 #text_change 13-Feb-1998

C/Accession: S24348

R/Moore, L.A.; Arrizubieta, M.J.; Tidyman, W.E.; Herman, L.A.; Bandman, E.

J. Mol. Biol. 225, 1143-1151, 1992

A:Title: Analysis of the chicken fast myosin heavy chain family. Localization of isoform

A:Reference number: S24348; MUID:92309413; PMID:1377278

A:Accession: S24348

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-955 <MOO>

A:Cross-references: EMBL:M74085

C:Superfamily: myosin heavy chain; myosin motor domain homology

C:Keywords: ATP; coiled coil; muscle contraction; skeletal muscle; thick filament

Query Match

Best Local Similarity 23.7%; Score 60; DB 2; Length 955;

Matches 14; Conservative 8; Mismatches 9; Indels 2; Gaps 1;

Oy 21 KEDNVLVESHEKSLG--EANKADVNVLTAKSQ 51

|| | | | | | | | | | | | | | | | | | | | |

Db 13 KEKKALQEAHQOTLDDQLQAEEDKVNTLTAKTK 45

Search completed: October 9, 2003, 08:14:29

Job time : 19.2687 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2003, 08:08:56 ; Search time 9.89552 Seconds
(without alignments)
242.368 Million cell updates/sec

Title: US-09-928-048A-5
Perfect score: 253
Sequence: 1 FVALGAPLAPRDAGSQRPK.....KSLGEANKADVNLTKAKSQ 51

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	248	98.0	115	1 PTHY_HUMAN	P01270 homo sapien
2	241	95.3	115	1 PTH_MACFA	Q9X335 macaca fasc
3	206	81.4	115	1 PTHY_CANFA	P52212 canis fami
4	199	78.7	115	1 PTHY_BOVIN	P01268 bos taurus
5	194	76.7	115	1 PTHY_PIG	P01269 sus scrofa
6	160	63.2	115	1 PTHY_RAT	P04089 rattus norv
7	68.5	27.1	119	1 PTHY_CHICK	P15743 gallus gall
8	63	24.9	1937	1 MYH8_HUMAN	P13535 homo sapien
9	61.5	24.3	366	1 YE05_HAEIN	P44180 haemophilus
10	60.5	23.9	555	1 UL25_HSV62	P02537 human herpe
11	60	23.7	1084	1 MYSS_RABIT	P02582 oryctolagus
12	60	23.7	1935	1 MYSS_CYPCA	Q90339 cyprinus ca
13	60	23.7	1938	1 MYH4_RABIT	Q28641 oryctolagus
14	60	23.7	1940	1 MYH3_CHICK	P02565 gallus gall
15	58.5	23.1	527	1 ATRX_RAT	P70486 rattus norv
16	58	22.9	465	1 MYH6_RABIT	P04460 oryctolagus
17	58	22.9	599	1 KLC2_MOUSE	O88448 mus musculu
18	58	22.9	1935	1 MYH7_HUMAN	P12883 homo sapien
19	58	22.9	1935	1 MYH7_PIG	P79293 sus scrofa
20	58	22.9	1935	1 MYH7_RAT	P02564 rattus norv
21	58	22.9	1939	1 MYH1_HUMAN	P12882 homo sapien
22	58	22.9	1941	1 MYH2_HUMAN	Q9UKX2 homo sapien
23	57.5	22.7	378	1 UL25_HSV6G	P52536 human herpe
24	57.5	22.7	555	1 UL25_HSV6U	P52387 human herpe
25	57	22.5	1939	1 MYH4_HUMAN	Q9Y623 homo sapien
26	56	22.1	396	1 DPO4_CLOAB	Q97mb3 clostridium
27	56	22.1	1938	1 MYSS_CHICK	P13538 gallus gall
28	55.5	21.9	2426	1 SON_HUMAN	P18583 homo sapien
29	55	21.7	831	1 NFH_RAT	P16884 rattus norv
30	55	21.7	1154	1 KDGB_MESAU	Q64398 mesocricetu
31	55	21.7	1505	1 SCP2_RAT	O70608 rattus norv
32	55	21.7	1518	1 KKK1_YEAST	P34244 saccharomyc
33	55	21.7	1934	1 MYH7_MESAU	P13540 mesocricetu

RESULT 1				
PTHY_HUMAN				
ID	PTHY_HUMAN	STANDARD:	PRT:	115 AA.
AC	P01270;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Parathyroid hormone precursor (Parathyrin) (PTH) (Parathormone).			
GN	PTH.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
EN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=82150870; PubMed=6950381;			
RA	Hendy G.N., Kronenberg H.M., Potts J.T. Jr., Rich A.;			
RT	"Nucleotide sequence of cloned cDNAs encoding human preproparathyroid hormone."			
RL	Proc. Natl. Acad. Sci. U.S.A. 78:7365-7369(1981).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=83169834; PubMed=6220408;			
RA	Vasicek T.J., McCevitt B.E., Freeman M.W., Fennick B.J.,			
RT	Hendy G.N., Potts J.T. Jr., Rich A., Kronenberg H.M.;			
RL	"Nucleotide sequence of the human parathyroid hormone gene."			
RN	Proc. Natl. Acad. Sci. U.S.A. 80:2127-2131(1983).			
RN	[3]			
RP	SEQUENCE OF 26-37.			
RX	MEDLINE=74174967; PubMed=4833516;			
RA	Jacobs J.W., Kemper B., Niall H.D., Habener J.F., Potts J.T. Jr.;			
RT	"Structural analysis of human parathyroid hormone by a new microsequencing approach."			
RL	Nature 249:155-157(1974).			
RN	[4]			
RP	SEQUENCE OF 32-68.			
RX	MEDLINE=7411656; PubMed=4521809;			
RA	Niall H.D., Sauer R.T., Jacobs J.W., Keutmann H.T., Segre G.V.,			
RA	O'Riordan J.L.H., Aurbach G.D., Potts J.T. Jr.;			
RT	"The amino-acid sequence of the amino-terminal 37 residues of human parathyroid hormone."			
RL	Proc. Natl. Acad. Sci. U.S.A. 71:384-388(1974).			
RN	[5]			
RP	SEQUENCE OF 61-83 AND 84-115.			
RX	MEDLINE=79082855; PubMed=728431;			
RA	Keutmann H.T., Sauer M.M., Hendy G.N., O'Riordan J.L.H.,			
RA	Potts J.T. Jr.;			
RT	"Complete amino acid sequence of human parathyroid hormone."			
RL	Biochemistry 17:5723-5729(1978).			
RN	[6]			
RP	SEQUENCE OF 75-100.			
RA	Keutmann H.T., Niall H.D., Jacobs J.W., Barling P.M., Hendy G.N.,			
RA	O'Riordan J.L.H., Potts J.T. Jr.;			
RT	(In) Talmadge R.V., Owen M., Parsons J.A. (eds.);			
RL	Calcium-regulating hormones, pp.9-14, Excerpta Medica Foundation, Amsterdam (1975).			

ALIGNMENTS

RN RP REVISIONS.
 RX MEDLINE=75146516; PubMed=1125201;
 RA Keutmann H.T., Niall H.D., O'Riordan J.L.H., Potts J.T. Jr.;
 RT "A reinvestigation of the amino-terminal sequence of human
 RL parathyroid hormone."
 RN Biochemistry 14:1842-1847(1975).
 [8]
 RN SYNTHESIS OF 32-65.
 RX MEDLINE=75059220; PubMed=4474131;
 RA Tregear G.W., van Riettschoten J., Green E., Niall H.D.,
 RA Keutmann H.T., Parsons J.A., O'Riordan J.L.H., Potts J.T. Jr.;
 RT "Solid-phase synthesis of the biologically active N-terminal 1-34
 RL peptide of human parathyroid hormone."
 RN Hoppe-Seyler's Z. Physiol. Chem. 355:415-421(1974).
 [9]
 RN SYNTHESIS OF 32-65.
 RX MEDLINE=73227467; PubMed=4721748;
 RA Andreatta R.H., Hartmann A., Joehl A., Kamber B., Maier R.,
 RA Riniker B., Rittel W., Sieber P.;
 RT "Synthesis of sequence 1-34 of human parathyroid hormone."
 RL Helv. Chim. Acta 56:470-473(1973).
 [10]
 RN STRUCTURE BY NMR OF 32-65.
 RX MEDLINE=91299748; PubMed=2069952;
 RA Klaus W., Dieckmann T., Wray V., Schomburg D., Wingender E., Mayer H.;
 RT "Investigation of the solution structure of the human parathyroid
 RL hormone fragment (1-34) by 1H NMR spectroscopy, distance geometry,
 and molecular dynamics calculations."
 RN Biochemistry 30:6936-6942(1991).
 [11]
 RN STRUCTURE BY NMR OF 32-65.
 RX MEDLINE=93345518; PubMed=8344299;
 RA Barden J.A., Cuthbertson R.M.;
 RT "Stabilized NMR structure of human parathyroid hormone(1-34).";
 RL Eur. J. Biochem. 215:315-321(1993).
 [12]
 RN STRUCTURE BY NMR OF 32-68.
 RX MEDLINE=95318084; PubMed=7797503;
 RA Marx U.C., Austermann S., Bayer P., Adermann K., Eichert A.,
 RA Sticht H., Walter S., Schmid F.-X., Jaenicke R., Forssmann W.-G.,
 RA Roesch P.;
 RT "Structure of human parathyroid hormone 1-37 in solution.";
 RL J. Biol. Chem. 270:15194-15202(1995).
 [13]
 RN STRUCTURE BY NMR OF 32-70.
 RX MEDLINE=20090619; PubMed=10623601;
 RA Marx U.C., Adermann K., Bayer P., Forssmann W.-G., Rosch P.;
 RT "Solution structures of human parathyroid hormone fragments
 RL hPTH(1-34) and hPTH(1-39) and bovine parathyroid hormone fragment
 bPTH(1-37).";
 RN Biochem. Biophys. Res. Commun. 267:213-220(2000).
 [14]
 RN VARIANT ARG-18.
 RX MEDLINE=91009811; PubMed=2212001;
 RA Arnold A., Horst S.A., Gardella T.J., Baba H., Levine M.A.,
 RA Kronenberg H.M.;
 RT "Mutation of the signal peptide-encoding region of the
 RL preproparathyroid hormone gene in familial isolated
 RT hypoparathyroidism.";
 RL J. Clin. Invest. 86:1084-1087(1990).
 CC -J- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 CC BONE AND PREVENTING THEIR RENAL EXCRETION.
 CC -I- DISEASE: Defects in PTH are a cause of familial isolated
 CC hypoparathyroidism (FHH) [MIM:146200].
 CC -I- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>)

or send an email to license@isb-sib.ch.

CC EMBL; J00301; AAA60215.1;
 DR EMBL; V00597; CAA23843.1;
 DR EMBL; A29146; CAA01956.1;
 DR PIR; A19339; PTHU.
 DR PDB; 1HPH; 10-JUL-95
 DR PDB; 1HTH; 15-OCT-97.
 DR PDB; 1ZWA; 12-MAR-97.
 DR PDB; 1ZWB; 12-MAR-97.
 DR PDB; 1ZWD; 12-MAR-97.
 DR PDB; 1ZWE; 12-MAR-97.
 DR PDB; 1ZWF; 16-JUN-97.
 DR PDB; 1ZWG; 16-JUN-97.
 DR PDB; 1ZWX; 14-JAN-00.
 DR PDB; 1HPY; 14-JAN-00.
 DR PDB; 1ET1; 06-SEP-00.
 DR PDB; 1ET2; 06-SEP-00.
 DR PDB; 1FVY; 31-DEC-02.
 DR Genew; HGNC:9606; PTH.
 DR MIM; 168450;
 DR MIM; 146200;
 DR GO; GO:0008492; F:camp generating peptide activity; TAS.
 DR GO; GO:0005180; F:peptide hormone; TAS.
 DR GO; GO:0007267; P:cell-cell signaling; TAS.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . ; TAS.
 DR GO; GO:0008628; P:induction of apoptosis by hormones; TAS.
 DR GO; GO:0001501; P:skeletal development; TAS.
 DR InterPro; IPR001415; Parathyroid_hrm.
 DR InterPro; IPR003625; Pthyhorm_sub.
 DR Pfam; PF01279; Parathyroid; 1.
 DR ProDom; PD010687; Pthyhorm_sub; 1.
 DR SMART; SM00087; PTH; 1.
 DR PROSITE; PS00335; PARATHYROID; 1.
 KW Hormone; Signal; Disease mutation; 3D-structure.
 FT SIGNAL 1 25
 FT PROPEP 26 31
 FT CHAIN 32 115
 FT VARIANT 18
 FT
 FT CONFLICT 107 107
 FT HELIX 36 41
 FT TURN 42 43
 FT HELIX 49 63
 FT TURN 64 66
 FT SEQUENCE 115 AA; 12861 MW; 849015736A6E5597 CRC64;
 Query Match 98.0%; Score 248; DB 1; Length 115;
 Best Local Similarity 98.0%; Pred. No. 1.9e-23;
 Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 N -> D (IN REF. 5).
 C -> R (IN FHH; LEADS TO INEFFICIENT
 PROCESSING OF THE PRECURSOR).
 /FTID=VAR_006047.
 N -> D (IN REF. 5).
 Qy 1 FVALGAPLAPDAGSQRPKRKEDNVLVESHEKSLGEAKADVNLTKRSQ 51
 Db 65 FVALGAPLAPDAGSQRPKRKEDNVLVESHEKSLGEAKADVNLTKRSQ 115
 RESULT 2
 ID PTH_MACFA STANDARD; PRT; 115 AA.
 AC Q9XT35;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Parathyroid hormone precursor (Parathyrin) (PTH).
 GN PTH.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Malaivijitnond S., Takenaka O.;
 RT "Nucleotide sequences of parathyroid gene in five species of macaque
 of Thailand.";
 RL J. Sci. Res. Chulalongkorn Univ. 23:135-142(1998).
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 CC BONE AND PREVENTING THEIR RENAL EXCRETION.
 CC -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>,
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AF130257; AAD2777.1; -;
 DR HSSP: P01270; LHPY;
 DR InterPro: IPR001415; Parathyrd_hrm.
 DR Pfam: PF01279; Parathyroid; 1.
 DR ProDom: PD010687; Pthyrdorm_sub; 1.
 DR SMART: SM00087; PTH; 1.
 DR PROSITE: PS00335; PARATHYROID; 1.
 KW Hormone; Signal.
 FT SIGNAL 1 25 BY SIMILARITY.
 FT PROPEP 26 31 BY SIMILARITY.
 FT CHAIN 32 115 PARATHYROID HORMONE.
 SQ SEQUENCE 115 AA; 12890 MW; 8C2500EF24BE5597 CRC64;
 Query Match 95.3%; Score 241; DB 1; Length 115;
 Best Local Similarity 92.2%; Pred. No. 1.3e-22;
 Matches 47; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 OY 1 FVALGAPLAPRDAGSQPRKKEDNVLVESHSKSLGKANKADVNLTKAKSQ 51
 Db 65 FVALGAPLAPRDAGSQPRKKEDNVLVESHSKSLGKANKADVNLTKAKSQ 115
 RESULT 3
 PTHY_CANFA
 ID PTHY_CANFA STANDARD; PRT; 115 AA.
 AC P52212;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Parathyroid hormone precursor (Parathyrlin) (PTH).
 GN PTH.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Parathyroid;
 RA Rosol T.J., Steinmeyer C.L., McCauley L.K., Groene A.,
 RA DeWille J.W., Capen C.C.;
 RT "Sequences of the cDNAs encoding canine parathyroid hormone-related
 RT protein and parathyroid hormone.";
 RL Gene 160:241-243(1995).
 CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
 CC BONE AND PREVENTING THEIR RENAL EXCRETION.
 CC -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>,
 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL: U15662; AAA82584.1; -;
 DR PIR: JC4202; JC4202.
 DR HSSP: P01268; IZWC.
 DR InterPro: IPR001415; Parathyrd_hrm.
 DR InterPro: IPR003625; Pthyrdorm_sub.
 DR Pfam: PF01279; Parathyroid; 1.
 DR ProDom: PD010687; Pthyrdorm_sub; 1.
 DR SMART: SM00087; PTH; 1.
 DR PROSITE: PS00335; PARATHYROID; 1.
 KW Hormone; Signal.
 FT SIGNAL 1 25 BY SIMILARITY.
 FT PROPEP 26 31 BY SIMILARITY.
 FT CHAIN 32 115 PARATHYROID HORMONE.
 SQ SEQUENCE 115 AA; 12957 MW; FC38F77F1C8CFE56 CRC64;
 Query Match 81.4%; Score 206; DB 1; Length 115;
 Best Local Similarity 82.4%; Pred. No. 2.5e-18;
 Matches 42; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
 OY 1 FVALGAPLAPRDAGSQPRKKEDNVLVESHSKSLGKANKADVNLTKAKSQ 51
 Db 65 FVALGAPLAPRDAGSQPRKKEDNVLVESHSKSLGKANKADVNLTKAKSQ 115
 RESULT 4
 PTHY_BOVIN
 ID PTHY_BOVIN STANDARD; PRT; 115 AA.
 AC P01268;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Parathyroid hormone precursor (Parathyrlin) (PTH).
 GN PTH.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kronenberg H.M., McDavitt B.E., Majzoub J.A., Nathans J., Sharp P.A.,
 RA Potts J.T. Jr., Rich A.;
 RT "Cloning and nucleotide sequence of DNA coding for bovine
 RT preproparathyroid hormone.";
 RL Proc. Natl. Acad. Sci. U.S.A. 76:4981-4985(1979).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=82037785; PubMed=6170060;
 RA Weaver C.A., Gordon D.F., Kemper B.;
 RT "Introduction by molecular cloning of artifactual inverted sequences
 RT at the 5' terminus of the sense strand of bovine parathyroid hormone
 RT cDNA.";
 RL Mol. Cell. Endocrinol. 28:411-424(1982).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=82037785; PubMed=6170060;
 RA Weaver C.A., Gordon D.F., Kemper B.;
 RT "Introduction by molecular cloning of artifactual inverted sequences
 RT at the 5' terminus of the sense strand of bovine parathyroid hormone
 RT cDNA.";
 RL Mol. Cell. Endocrinol. 28:411-424(1982).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84262483; PubMed=6086460;
 RA Weaver C.A., Gordon D.F., Kissil M.S., Mead D.A., Kemper B.;
 RT "Isolation and complete nucleotide sequence of the gene for bovine
 RT parathyroid hormone.";
 RL Gene 28:319-329(1984).
 RN [5]
 RP SEQUENCE OF 26-115.
 RX MEDLINE=74142666; PubMed=4522780;
 RA Hamilton J.W., Niall H.D., Jacobs J.W., Keutmann H.T., Potts J.T. Jr.,
 RA Cohn D.V.;
 RT "The N-terminal amino-acid sequence of bovine preparathyroid

hormone.";

RT Proc. Natl. Acad. Sci. U.S.A. 71:653-656(1974).

[6]

SEQUENCE OF 32-115.

RA Niall H.D., Keutmann H.T., Sauer R., Hogan M.L., Dawson B.F.,

RX MEDLINE=71076162; PubMed=5531031;

RA Aurbach G.D., Fotts J.T. Jr.;

RT "The amino acid sequence of bovine parathyroid hormone I.";

RA Hoppe-Seyler's Z. Physiol. Chem. 351:1586-1588(1970).

[7]

SEQUENCE OF 32-115.

RA MEDLINE=71063634; PubMed=5275384;

RX MEDLINE=71091588; PubMed=4322265;

RA Potts J.T. Jr., Tregear G.W., Keutmann H.T., Niall H.D., Sauer R.,

RX Deftos L.J., Dawson B.F., Hogan M.L., Aurbach G.D.;

RA "Synthesis of a biologically active N-terminal tetraoctapeptide

RT of parathyroid hormone.";

RT Proc. Natl. Acad. Sci. U.S.A. 67:1862-1869(1970).

[8]

SYNTHESIS OF 32-65.

RA MEDLINE=71091588; PubMed=4322265;

RX MEDLINE=71091588; PubMed=4322265;

RA Potts J.T. Jr., Tregear G.W., Keutmann H.T., Niall H.D., Sauer R.,

RX Deftos L.J., Dawson B.F., Hogan M.L., Aurbach G.D.;

RA "Synthesis of a biologically active N-terminal tetraoctapeptide

RT of parathyroid hormone.";

RT Proc. Natl. Acad. Sci. U.S.A. 67:1862-1869(1970).

[9]

STRUCTURE BY NMR OF 32-68.

RA MEDLINE=20090619; PubMed=10623601;

RX MEDLINE=20090619; PubMed=10623601;

RA Marx U.C., Ademmann K., Beyer P., Forssmann W.-G., Rosch P.;

RX "Solution structures of human parathyroid hormone fragments

RT hPTH(1-34) and hPTH(1-39) and bovine parathyroid hormone fragment

RT bPTH(1-37)".

RT Biochem. Biophys. Res. Commun. 267:213-220(2000).

CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN

CC BONE AND PREVENTING THEIR RENAL EXCRETION.

CC -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>

CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; V00106; CAA23439.1; -

DR EMBL; J00024; AAA30747.1; -

DR EMBL; K01938; AAA30749.1; -

DR EMBL; M25082; AAA30748.1; -

DR PIR; A24949; PTBO.

DR PDB; 1ZWC; 12-MAR-97.

DR InterPro; IPR001415; Parathyrd_hrm.

DR InterPro; IPR003625; Pthyrhorm_sub.

DR Pfam; PF01279; Parathyroid; 1.

DR ProDom; PD010687; Pthyrhorm_sub; 1.

DR SMART; SM00087; PTH; 1.

DR PROSITE; PS00335; PARATHYROID; 1.

KW Hormone; Signal; 3D-structure.

FT SIGNAL 1 25

FT PROPEP 26 31

FT CHAIN 32 115 PARATHYROID HORMONE.

FT CONFLICT 106 106 V -> G (IN REF. 4).

FT HELIX 37 40

FT TURN 41 42

FT TURN 51 52

FT HELIX 53 63

FT TURN 61 63

SEQUENCE 115 AA; 12980 MW; 2ED245B348880710 CRC64;

Query Match 78.7%; Score 199; DB 1; Length 115;

Best Local Similarity 80.4%; Pred. No. 1.8e-17;

Matches 41; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSQRPKKEDNVLVPSHEKSLGKANKADVNVLTAKSQ 51

||||| : ||| ||||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

Db      65 FVALGASIAYDRGSSQRPRKKEDNVLVESHOKSLGEADKADVDVLIKAKPQ 115

RESULT 5
PTHY_PIG ID PTHY_PIG STANDARD; PRT: 115 AA.
AC PO1269;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1988 (Rel. 06, last sequence update)
DT 15-JUL-1998 (Rel. 36, last annotation update)
DE Parathyroid hormone precursor (Parathyrin) (PTH).
GN PTH.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
[1]
RN MEDLINE=73116938; PubMed=3628009;
RA Schmelzer H.-J., Gross G., Widera G., Mayer H.:
RT "Nucleotide sequence of a full-length cDNA clone encoding
RT preproparathyroid hormone from pig and rat.";
RN Nucleic Acids Res. 15:6740-6740(1987).
[2]
RN MEDLINE=76018954; PubMed=1164500;
RA Chu L.L.H., Huang W.-Y., Littlelike E.T., Hamilton J.W., Cohn D.V.:
RT "Porcine parathyroid hormone. Identification, biosynthesis, an
RT partial amino acid sequence.";
RN Biochemistry 14:3631-3635(1975).
[3]
RN MEDLINE=74253317; PubMed=4840833;
RA Sauer R.T., Niall H.D., Hogan M.B., Keutmann H.T., O'Riordan J.L.
RA Potts J.F. Jr.;
RT "The amino acid sequence of porcine parathyroid hormone.";
RN Biochemistry 13:1994-1999(1974).
CC 1! FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
CC 1! SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a colla
CC between the Swiss Institute of Bioinformatics and the EMBL outpu
CC the European Bioinformatics Institute. There are no restrictions o
CC use by non-profit institutions as long as its content is in
CC modified and this statement is not removed. Usage by and for co
CC entities requires a license agreement (See http://www.isb-sib.ch/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL; X05722; CAA29193.1;
DR PIR; B26806; PTPG.
DR HSP; P01270; IBMX.
DR InterPro; IPR001415; Parathyrd_hrm.
DR InterPro; IPR003625; Pthyorm_sub.
DR Pfam; PF01279; Parathyroid; 1.
DR ProDom; PD010687; Pthyorm_sub; 1.
DR SMART; SM00087; PTH; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
KW Hormone; Signal.
FT SIGNAL 1 25
FT FT 26 31
FT PROPEP 32 115
FT CHAIN 115 AA; 12852 MW; 9FE8BCDE614BAC16 CRC64;
SQ SEQUENCE 115 AA; 12852 MW; 9FE8BCDE614BAC16 CRC64;

Query Match 76.7% Score 194; DB 1; Length 115;
Best Local Similarity 78.4%; Pred. No. 7.3e-17;
Matches 40; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 FVALGAPLAFPDAGSQRPRKKEDNVLVESHSKEAGANKADVNLVTAKSQ 51
||||| : || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
65 FVALGASIVHRDGSQRPRKKEDNVLVESHOKSLGEADKADVDVLIKAKPQ 115

```

RESULT 6

PTHY_RAT STANDARD; PRT; 115 AA.

AC P04089; 063473;

DT 01-NOV-1986 (Rel. 03, Created)

DT 01-NOV-1986 (Rel. 03, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Parathyroid hormone precursor (Parathyrin) (PTH).

GN PTH.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=84135846; PubMed=6321505;

RA Heinrich G., Kronenberg H.M., Potts J.T. Jr., Habener J.F.;

RT "Gene encoding parathyroid hormone. Nucleotide sequence of the rat

RT gene and deduced amino acid sequence of rat preproparathyroid

RT hormone.";

RL J. Biol. Chem. 259:3320-3329(1984).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=87316938; PubMed=3628009;

RA Schmelzer H.-J., Gross G., Widera G., Mayer H.;

RT "Nucleotide sequence of a full-length cDNA clone encoding

RT preproparathyroid hormone from pig and rat.";

RL Nucleic Acids Res. 15:6740-6740(1987).

RN [3]

RP SEQUENCE OF 10-115 FROM N.A.

RC TISSUE=Parathyroid;

RA Schmelzer H.-J., Gross G., Mayer H.;

RT "Nucleotide sequence of cloned cDNA encoding rat prepro parathyroid

RT hormone.";

RL Adv. Gene Technol. 21:228-229(1984).

RN [4]

RP SEQUENCE OF 32-115 FROM N.A.

RC STRAIN=Sprague-Dawley; TISSUE=Brain, Liver, and Parathyroid;

RX MEDLINE=96079910; PubMed=758314;

RA Nutley M.T., Pazimi S.A., Harvey S.;

RT "Sequence analysis of hypothalamic parathyroid hormone messenger

RT ribonucleic acid.";

RL Endocrinology 136:5600-5607(1995).

CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN

CC BONE AND PREVENTING THEIR RENAL EXCRETION.

CC -1- TISSUE SPECIFICITY: HYPOTHALAMUS AND PARATHYROID GLAND.

CC -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.

CC

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC

DR EMBL; K01268; AAA41979.1; -

DR EMBL; X05721; CAA29192.1; -

DR EMBL; M54875; AAA57156.1; -

DR EMBL; S80127; -; NOT_ANNOTATED_CDS.

DR PIR; A05091; A05091.

DR HSP; P01270; 12WB.

DR InterPro; IPR001415; Parathyrd_hrm.

DR InterPro; IPR003625; pthyrdorm_sub.

DR Pfam; PF01279; Parathyroid; 1.

DR ProDom; PD010687; pthyrdorm_sub; 1.

DR SMART; SM00087; PTH; 1.

DR PROSITE; PS00335; PARATHYROID; 1.

KW Hormone; Signal.

FT SIGNAL 1 25

FT PROPEP 26 31

FT CHAIN 32 115 PARATHYROID HORMONE.

FT CONFLICT 18 18 C -> Y (IN REF. 3).

FT CONFLICT 23 23 A -> T (IN REF. 3).

FT CONFLICT 33 33 V -> I (IN REF. 3).

FT CONFLICT 62 62 V -> G (IN REF. 3).

SQ SEQUENCE 115 AA; 12722 MW; 7B434CFC5A28B230 CRC64;

Query Match 63.2%; Score 160; DB 1; Length 115;

Best Local Similarity 62.7%; Pred. No. 1e-12; Indels 0; Gaps 0;

Matches 32; Conservative 8; Mismatches 11;

Oy 1 FVALGAPLAPRDAGSORPRKEDNVLVESHEKSLGKANKADVNVLTAKSQ 51

Db 65 FVSLGVQMAAREGSYQRTKKEENVLYDGNKSLGKADVDVLVKAKSQ 115

RESULT 7

PTHY_CHICK STANDARD; PRT; 119 AA.

AC P15743;

DT 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE Parathyroid hormone precursor (PTH).

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCBI_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=89219100; PubMed=2710135;

RA Russell J., Sherwood L.M.;

RT "Nucleotide sequence of the DNA complementary to avian (chicken)

RT preproparathyroid hormone mRNA and the deduced sequence of the

RT hormone precursor.";

RL Mol. Endocrinol. 3:325-331(1989).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=89284968; PubMed=3251402;

RA Khosla S., Demay M., Pines M., Hurwitz S., Potts J.T. Jr.;

RA Kronenberg H.M.;

RT "Nucleotide sequence of cloned cDNAs encoding chicken

RT preproparathyroid hormone.";

RL J. Bone Miner. Res. 3:689-698(1988).

CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN

CC BONE AND PREVENTING THEIR RENAL EXCRETION.

CC -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.

CC

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC

DR EMBL; M31504; AAA49093.1; -

DR EMBL; M36522; AAB02866.1; -

DR PIR; A34937; A34937.

DR HSP; P01270; 1HPY.

DR InterPro; IPR001415; Parathyrd_hrm.

DR InterPro; IPR003625; pthyrdorm_sub.

DR Pfam; PF01279; Parathyroid; 1.

DR ProDom; PD010687; pthyrdorm_sub; 1.

DR SMART; SM00087; PTH; 1.

DR PROSITE; PS00335; PARATHYROID; 1.

KW Hormone; Signal.

FT SIGNAL 1 25

FT PROPEP 26 31

FT CHAIN 32 119 PARATHYROID HORMONE.

FT CONFLICT 119 AA; 13943 MW; B309D8E772997F6E CRC64;

Query Match 27.1%; Score 68.5; DB 1; Length 119;

Best Local Similarity 38.9%; Pred. No. 0.16;

Matches 21: Conservative 6; Mismatches 14; Indels 13; Gaps 1;

QY 9 APRDAGSQRKKEDNVLVE-----SHEKSLGEANKADVNLTKAK 49
 DB 65 ALEDARTQPRNKEDIVLGEIRNRRLPEHLRAAVOKKSIDLDRAYNNVLPFTK 118

RESULT 8
 MYH8_HUMAN
 ID MYH8_HUMAN STANDARD; PRT; 1937 AA.
 AC P13535; Q14910;
 DT 01-JAN-1990 (Rel. 13, Created)
 DE 15-JUL-1998 (Rel. 36, Last sequence update)
 DE 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Myosin heavy chain, skeletal muscle, perinatal (MYHC-perinatal).
 GN MYH8.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID-9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Skeletal muscle;
 RX MEDLINE-90323631; PubMed-2373371;
 RA Karsch-Mizrachi I., Feghalli R., Shows T.B. Jr., Leinwand L.A.;
 RT "Generation of a full-length human perinatal myosin heavy-chain-
 RT encoding cDNA.";
 RL Gene 89:289-294(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Skeletal muscle;
 RX MEDLINE-95324556; PubMed-7601129;
 RA Jullian E.H., Kelly A.M., Pompidou A.J., Hoffman R., Schiaffino S.,
 RA Stedman H.H., Rubinstein N.A.;
 RT "Characterization of a human perinatal myosin heavy-chain
 RT transcript.";
 RL Eur. J. Biochem. 230:1001-1006(1995).
 RN [3]
 RP SEQUENCE OF 502-1937 FROM N.A.
 RC TISSUE-Skeletal muscle;
 RX MEDLINE-90235862; PubMed-1691980;
 RA Bober E., Buchberger-Seidl A., Braun T., Singh S., Goedde H.W.,
 RA Arnold H.H.;
 RT "Identification of three developmentally controlled isoforms of human
 RT myosin heavy chains.";
 RL Eur. J. Biochem. 189:55-65(1990).
 RN [4]
 RP SEQUENCE OF 860-1937 FROM N.A.
 RX MEDLINE-89234168; PubMed-2715179;
 RA Feghalli R., Leinwand L.A.;
 RT "Molecular genetic characterization of a developmentally regulated
 RT human perinatal myosin heavy chain.";
 RL J. Cell Biol. 108:1791-1797(1989).
 RN [5]
 RP SEQUENCE OF 1-46 FROM N.A.
 RA Esser K., Tidhar A., Wyszowski M.;
 RT "Isolation and characterization of the human perinatal MHC promoter.";
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.

-1- FUNCTION: MUSCLE CONTRACTION.
 CC -1- SUBUNIT: MYOSIN MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
 CC HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
 CC AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MUC-2).
 CC -1- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
 CC CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
 CC CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
 CC -1- PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY
 CC ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
 CC -1- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
 CC MEROMYOSIN (LM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE
 CC SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
 CC SUBFRAGMENT (S2).
 CC -1- SIMILARITY: Contains 1 myosin-like globular head domain.

CC CC -1- SIMILARITY: Contains 1 IQ domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M36769; AAC17185.1; -
 DR EMBL; Z38133; CAA86293.1; -
 DR EMBL; X51592; CAA35941.1; -
 DR EMBL; AF067143; AAC21557.1; -
 DR PIR; I38055; I38055.
 DR HSSP; P13538; 2MYS.
 DR Genes; HGNC:7578; MYH8.
 DR MIN; 160741; -
 DR GO; GO:0005859; C:muscle myosin; TAS.
 DR GO; GO:0008307; F:structural constituent of muscle; TAS.
 DR InterPro; IPR000048; IQ_region.
 DR InterPro; IPR001609; Myosin_head.
 DR InterPro; IPR004009; Myosin_N.
 DR InterPro; IPR002928; Myosin_tail.
 DR Pfam; PF00612; IQ; 1.
 DR Pfam; PF00063; myosin_head; 1.
 DR Pfam; PF02736; Myosin_N; 1.
 DR Pfam; PF01576; Myosin_tail; 1.
 DR PRINTS; PR00193; MYOSINHEAVY.
 DR ProDom; PD000355; myosin_head; 1.
 DR SMART; SM00015; IQ; 1.
 DR SMART; SM00242; MYSC; 1.
 DR PROSITE; PS50096; IQ; 1.
 KW Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;
 KW ATP-binding; Methylation; Alkylation; Multigene family;
 KW Calmodulin-binding.
 FT DOMAIN 1 780 MYOSIN HEAD-LIKE.
 FT DOMAIN 781 813 IQ.
 FT DOMAIN 842 1937 COILED COIL (POTENTIAL).
 FT NP_BIND 181 188 ATP.
 FT DOMAIN 658 680 ACTIN-BINDING.
 FT DOMAIN 760 774 ACTIN-BINDING.
 FT MOD_RES 132 132 METHYLATION (TRI-) (POTENTIAL).
 FT MOD_RES 698 698 ALKYLATION (SH-1) (POTENTIAL).
 FT MOD_RES 708 708 ALKYLATION (SH-2) (POTENTIAL).
 FT CONFLICT 15 15 A -> R (IN REF. 2).
 FT CONFLICT 970 970 E -> Q (IN REF. 1 AND 4).
 FT CONFLICT 1072 1072 M -> N (IN REF. 3).
 FT CONFLICT 1247 1247 N -> H (IN REF. 1 AND 4).
 FT CONFLICT 1251 1252 MC -> DGG (IN REF. 3).
 FT CONFLICT 1261 1261 E -> G (IN REF. 1 AND 4).
 FT CONFLICT 1297 1297 K -> Q (IN REF. 1 AND 4).
 FT CONFLICT 1377 1378 KY -> NT (IN REF. 3).
 FT CONFLICT 1504 1505 EN -> AH (IN REF. 1 AND 4).
 FT CONFLICT 1847 1847 E -> D (IN REF. 1 AND 4).
 FT CONFLICT 1914 1914 D -> H (IN REF. 2).
 SQ SEQUENCE 1937 AA; 222762 MW; A3EE2D151792E9E8 CRC64;
 Query Match 24.98; Score 63; DB 1; Length 1937;
 Best Local Similarity 42.4%; Pred. No. 16;
 Matches 14; Conservative 9; Mismatches 8; Indels 2; Gaps 1;
 QY 21 KEDNLVESHEKSLG--EANKADVNLTKAKSO 51
 DB 997 KEKALQETHQQTLDLQAEEDKVNLTAKTK 1029
 RESULT 9
 ID YE05_HAEIN STANDARD; PRT; 366 AA.
 AC P44150;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=New Zealand white; TISSUE=Skeletal muscle;
 RA Maeda K., Hostinova E., Roesch-Kleinhauf A., Schuster H., Gasperik J.,
 RA Wittinghofer A.;
 RT "Isolation, sequencing of myosin heavy chain cDNA from rabbit
 RT skeletal muscle and a novel cosynthesis of S-1 fragment with the
 RT essential and regulatory light chains.";
 RL Submitted (Aug-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: MUSCLE CONTRACTION.
 CC -1- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
 CC HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC).
 CC AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
 CC -1- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
 CC CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
 CC CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
 CC -1- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
 CC MEROMYOSIN (LMN) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE
 CC SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
 CC SUBFRAGMENT (S2).
 CC -1- SIMILARITY: Contains 1 myosin-like globular head domain.
 CC -1- SIMILARITY: Contains 1 IQ domain.
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U32574; AAA74199.1;
 DR PIR: A59293; A59293.
 DR HSSP: P13538; 2MYS.
 DR InterPro: IPR0000048; IQ_region.
 DR InterPro: IPR001609; myosin_head.
 DR InterPro: IPR004009; Myosin_N.
 DR InterPro: IPR002928; Myosin_tail.
 DR Pfam: PF00612; IQ; 2.
 DR Pfam: PF00063; myosin_head; 1.
 DR Pfam: PF02736; Myosin_N; 1.
 DR Pfam: PF01576; Myosin_tail; 1.
 DR PRINTS: PR00193; MYOSINHEAVY.
 DR ProDom: PD000355; myosin_head; 1.
 DR SMART: SM00015; IQ; 1.
 DR SMART: SM00242; MYSC; 1.
 DR PROSITE: PS50096; IQ; 1.
 DR Calmodulin-binding; ATP-binding; Methylation; Alkylation;
 KW Multigene family.
 FT DOMAIN 1 783 MYOSIN HEAD-LIKE.
 FT DOMAIN 784 813 IQ.
 FT DOMAIN 842 1938 COILED COIL (POTENTIAL).
 FT NP_BIND 179 186 ATP (POTENTIAL).
 FT DOMAIN 658 680 ACTIN-BINDING (BY SIMILARITY).
 FT DOMAIN 760 774 ACTIN-BINDING (BY SIMILARITY).
 FT MOD_RES 35 METHYLATION (MONO-) (BY SIMILARITY).
 FT MOD_RES 130 METHYLATION (TRI-) (BY SIMILARITY).
 FT MOD_RES 552 METHYLATION (TRI-) (BY SIMILARITY).
 FT MOD_RES 756 METHYLATION (TRI-) (BY SIMILARITY).
 FT MOD_RES 698 ALKYLATION (SH-1) (BY SIMILARITY).
 FT MOD_RES 708 ALKYLATION (SH-2) (BY SIMILARITY).
 SQ SEQUENCE 1938 AA; 223064 MW; D9A8A2EC5B182626 CRC64;
 Query Match 23.7%; Score 60; DB 1; Length 1938;
 Best Local Similarity 42.4%; Pred. No. 38;
 Matches 14; Conservative 8; Mismatches 9; Indels 2; Gaps 1;
 OY 21 KEDNVLVESKSLG--EANKADVNVLTAKSK 51

Db. 997 KEKKAQARHOOTLDDIQAEDKVNLTAKTK 1029
 RESULT 14
 ID MYH3_CHICK STANDARD; PRT; 1940 AA.
 AC P02565;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Myosin heavy chain, fast skeletal muscle, embryonic.
 GN MYH3.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87194881; PubMed=3571266;
 RA Molina M.I., Kropp K.E., Gulick J., Robbins J.;
 RT "The sequence of an embryonic myosin heavy chain gene and isolation
 RT of its corresponding cDNA".
 RL J. Biol. Chem. 262:6478-6488 (1987).
 RN [2]
 RP SEQUENCE OF 1502-1940 FROM N.A.
 RX MEDLINE=83161144; PubMed=6833296;
 RA Kavinsky C.J., Umeda P.K., Sinha A.M., Elzinga M., Tong S.W., Zak R.,
 RA Jakovic S., Rabinowitz M.;
 RT "Cloned mRNA sequences for two types of embryonic myosin heavy chains
 RT from chick skeletal muscle. I. DNA and derived amino acid sequence of
 RT light meromyosin".
 RL J. Biol. Chem. 258:5196-5205 (1983).
 CC -1- FUNCTION: MUSCLE CONTRACTION.
 CC -1- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
 CC HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC).
 CC AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
 CC -1- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
 CC CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
 CC CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
 CC -1- PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY
 CC ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
 CC -1- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
 CC MEROMYOSIN (LMN) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE
 CC SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
 CC SUBFRAGMENT (S2).
 CC -1- SIMILARITY: Contains 1 myosin-like globular head domain.
 CC -1- SIMILARITY: Contains 1 IQ domain.
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: V00430; CAA23712.1;
 DR EMBL: J02714; AAA48972.1;
 DR PIR: A29320; A29320.
 DR HSSP: P13538; 2MYS.
 DR InterPro: IPR000048; IQ_region.
 DR InterPro: IPR001609; myosin_head.
 DR InterPro: IPR004009; Myosin_N.
 DR InterPro: IPR002928; Myosin_tail.
 DR Pfam: PF00612; IQ; 2.
 DR Pfam: PF00063; myosin_head; 1.
 DR Pfam: PF02736; Myosin_N; 1.
 DR Pfam: PF01576; Myosin_tail; 1.
 DR PRINTS: PR00193; MYOSINHEAVY.
 DR ProDom: PD000355; myosin_head; 1.
 DR SMART: SM00015; IQ; 1.
 DR SMART: SM00242; MYSC; 1.
 DR PROSITE: PS50096; IQ; 1.
 DR Calmodulin-binding; ATP-binding; Methylation; Alkylation;
 KW Multigene family.
 FT DOMAIN 1 783 MYOSIN HEAD-LIKE.
 FT DOMAIN 784 813 IQ.
 FT DOMAIN 842 1938 COILED COIL (POTENTIAL).
 FT NP_BIND 179 186 ATP (POTENTIAL).
 FT DOMAIN 658 680 ACTIN-BINDING (BY SIMILARITY).
 FT DOMAIN 760 774 ACTIN-BINDING (BY SIMILARITY).
 FT MOD_RES 35 METHYLATION (MONO-) (BY SIMILARITY).
 FT MOD_RES 130 METHYLATION (TRI-) (BY SIMILARITY).
 FT MOD_RES 552 METHYLATION (TRI-) (BY SIMILARITY).
 FT MOD_RES 756 METHYLATION (TRI-) (BY SIMILARITY).
 FT MOD_RES 698 ALKYLATION (SH-1) (BY SIMILARITY).
 FT MOD_RES 708 ALKYLATION (SH-2) (BY SIMILARITY).
 SQ SEQUENCE 1938 AA; 223064 MW; D9A8A2EC5B182626 CRC64;

DR SMART; SM00015; IO: 1.
 DR SMART; SM00242; MYSC: 1.
 DR PROSITE; PS50096; IO: 1.
 KW Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;
 KW Calmodulin-binding; ATP-binding; Methylation; Alkylation;
 KW Multigene family.
 FT DOMAIN 1 785
 FT MYOSIN HEAD-LIKE.
 FT DOMAIN 786 815
 FT COILED COIL (POTENTIAL).
 FT NP_BIND 844 1940
 FT ATP.
 FT DOMAIN 179 186
 FT ACTIN-BINDING.
 FT DOMAIN 560 682
 FT ACTIN-BINDING.
 FT MOD_RES 762 776
 FT METHYLATION (SH-1).
 FT MOD_RES 130 130
 FT ALKYLATION (SH-2).
 FT MOD_RES 710 710
 FT ALKYLATION (SH-2).
 FT VARIANT 379 379
 FT G -> D. (IN REF. 2).
 FT CONFLICT 1547 1547
 FT CONFLICT 1913 1915
 FT ERA -> GRT (IN REF. 2).
 SQ SEQUENCE 1940 AA; 222816 MW; C34833D75B04DFF2 CRC64;
 Query Match 23.7%; Score 60; DB 1; Length 1940;
 Best Local Similarity 42.4%; Pred. No. 38;
 Matches 14; Conservative 8; Mismatches 9; Indels 2; Gaps 1;
 QY 21. KEDNVLVESHEKSLG--EANKADVNVLTAKSQ 51
 DB 999 KEKALQEAHQTLDDLQAEEDKVNLTAKTK 1031
 RESULT 15
 ATRX_RAT
 ID ATRX_RAT STANDARD; PRT; 527 AA.
 AC P70486;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Transcriptional regulator ATRX (X-linked nuclear protein) (PABP-2)
 DE (Fragment).
 GN ATRX.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RC STRAIN-Wistar; TISSUE-Embryonic brain;
 RX MEDLINE=96301899; PubMed=8667030;
 RA Ohsawa K., Imai Y., Ito D., Kohsaka S.;
 RT "Molecular cloning and characterization of annexin V-binding proteins
 with highly hydrophilic peptide structure";
 RL J. Neurochem. 67:89-97(1996).
 CC -1- FUNCTION: COULD BE A GLOBAL TRANSCRIPTIONAL REGULATOR. MODIFIES
 CC GENE EXPRESSION BY AFFECTING CHROMATIN.
 CC -1- SUBUNIT: PROBABLY BINDS EZH2. BINDS ANNEXIN V IN A CALCIUM AND
 CC PHOSPHATIDYLCHOLINE/PHOSPHATIDYLSELINE-DEPENDENT MANNER.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR. ASSOCIATED WITH PERICENTROMERIC
 CC HETEROCHROMATIN DURING INTERPHASE AND MITOSIS, PROBABLY BY
 CC INTERACTING WITH HP1 (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE SNF2/RAD54 HELICASE FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; D64059; BAA10936.1; -
 KW DNA repair; Nuclear protein; DNA-binding; Helicase.
 FT NON_TER 1 1
 FT DOMAIN 251 256 POLY-SER.
 FT DOMAIN 304 307 POLY-SER.

FT DOMAIN 360 367 POLY-ASP.
 FT NON_TER 527 527
 SQ SEQUENCE 527 AA; 59258 MW; ABEF4B10C086D638 CRC64;
 Query Match 23.1%; Score 58.5; DB 1; Length 527;
 Best Local Similarity 33.9%; Pred. No. 14;
 Matches 19; Conservative 7; Mismatches 17; Indels 13; Gaps 2;
 QY 9 APRDAGSORPRKKEDNV-----LVESHEKS-----LGANKADVNVLTAKSQ 51
 DB 18 AVSSAGSEKPSGKEENVHSPEDKRVTKSEKSKHLRTTGRKVKSDVTDTRFKKEQ 73
 Search completed: October 9, 2003, 08:11:22
 Job time : 10.8955 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2003, 08:08:56 ; Search time 45.6716 Seconds
(without alignments)
288.159 Million cell updates/sec

Title: US-09-928-048A-5
Perfect score: 253
Sequence: 1 FVALGAPLAPRDAGSQRP...KSLGEANKADVNLTKAKSQ 51

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_cheap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	205	81.0	115	6 Q9GL67	Q9GL67 felis silve
2	203	80.2	86	6 Q9N1V0	Q9N1V0 equus caball
3	158	62.5	115	11 Q9ZOL6	Q9ZOL6 mus musculus
4	65	25.7	283	9 Q9AZW5	Q9AZW5 bacterioph
5	65	25.7	283	16 Q9CFN5	Q9CFN5 lactococcus
6	63.5	25.1	487	10 Q23304	Q23304 arabidopsis
7	63	24.9	975	13 Q98TQ5	Q98TQ5 notothenia
8	63	24.9	1119	13 P87344	P87344 theragra ch
9	63	24.9	1287	13 Q93498	Q93498 theragra ch
10	63	24.9	1287	13 Q98TQ6	Q98TQ6 notothenia
11	61	24.1	565	16 Q99WCS	Q99WCS staphylococ
12	60	23.7	1092	13 Q90338	Q90338 cyprinus ca
13	60	23.7	1930	13 Q9DGD5	Q9DGD5 pennahia ar
14	60	23.7	1931	13 Q910C5	Q910C5 gallus gall
15	60	23.7	1931	13 Q42352	Q42352 cyprinus ca
16	60	23.7	1933	13 Q90337	Q90337 cyprinus ca

ALIGNMENTS

RESULT 1

Q9GL67 PRELIMINARY; PRT; 115 AA.
ID Q9GL67
AC Q9GL67
DT 01-MAR-2001 (TREMREL. 16, Created)
DT 01-MAR-2001 (TREMREL. 16, Last sequence update)
DT 01-JUN-2002 (TREMREL. 21, Last annotation update)
DE Preproparathyroid hormone precursor.
GN PTH.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Toribio R.E., Kohn C.W., Leone G.W., Capen C.C., Rosol T.J.;
RT "Molecular cloning of feline preproparathyroid hormone,";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF309967; AAC30545.1;
DR HSSP; P01268; IZWC.
DR InterPro; IPR001415; Parathyrd_hrm.
DR InterPro; IPR003625; Pthyrhorm_sub.
DR Pfam; PF01279; Parathyroid; 1.
DR ProDom; PD010687; Pthyrhorm_sub; 1.
DR SMART; SM00087; PTH; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
FT SIGNAL
FT CHAIN
SQ SEQUENCE 115 AA; 12921 MW; 80CD557CC6A1A47E CRC64;

Query Match 81.0%; Score 205; DB 6; Length 115;
Best Local Similarity 80.4%; Pred. No. 3.6e-18;
Matches 41; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 FVALGAPLAPRDAGSQRP...KSLGEANKADVNLTKAKSQ 51
Db 65 FVALGAPLAPRDAGSQRP...KSLGEANKADVNLTKAKSQ 115

17 60 23.7 1936 13 Q90YF6
18 60 23.7 1937 6 Q9TV62
19 60 23.7 1937 6 Q8MJV1
20 60 23.7 1938 6 Q8MJV0
21 60 23.7 1938 6 Q8BE40
22 60 23.7 1938 13 Q9IBD7
23 60 23.7 1939 6 Q9TV63
24 60 23.7 1939 6 Q9TV61
25 60 23.7 1940 6 Q8BE41
26 60 23.7 1940 13 Q8AY28
27 60 23.7 1941 13 Q9DGM4
28 60 23.7 1943 13 Q8JG72
29 60 23.7 1944 13 Q9DGM5
30 60 23.7 6994 5 Q17343
31 59.5 23.5 909 2 Q52585
32 59.5 23.5 909 2 Q52585
33 59.5 23.5 1400 5 Q9TYW5
34 59 23.3 462 2 Q05090
35 59 23.3 565 16 Q8NY08
36 59 23.3 823 16 Q8PBY4
37 59 23.3 1006 4 Q96I57
38 59 23.3 1889 4 Q9H430
39 59 23.3 2010 4 Q9P216
40 58.5 23.1 142 10 Q9M344
41 58.5 23.1 288 10 Q94G09
42 58 22.9 234 6 Q28829
43 58 22.9 258 4 Q92679
44 58 22.9 518 5 Q9VRP4
45 58 22.9 619 11 Q91Y54

Q90YF6 paracirrh
Q9TV62 sus scrofa
Q8MJV1 equus caball
Q8MJV0 equus caball
Q8BE40 bos taurus
Q9IBD7 seriola dum
Q9TV63 sus scrofa
Q9TV61 sus scrofa
Q8BE41 bos taurus
Q8AY28 gallus gall
Q9DGM4 gallus gall
Q8JG72 gallus gall
Q9DGM5 gallus gall
Q17343 caenorhabdi
Q17490 caenorhabdi
Q52585 pseudomonas
Q52585 pseudomonas
Q9TYW5 caenorhabdi
Q05090 nocardioid
Q8NY08 staphylococ
Q8PBY4 xanthomonas
Q96I57 homo sapien
Q9H430 homo sapien
Q9P216 homo sapien
Q9M344 arabidopsis
Q94G09 oryza sativ
Q28829 oryctolagus
Q92679 homo sapien
Q9VRP4 drosophila
Q91Y54 mus musculu


```

Matches 13; Conservative 8; Mismatches 15; Indels 0; Gaps 0;
QY 15 SQRPRKEDNVLVESHEKSLGEANKADNVNLTAKS 50
   : : : : : : : : : : : : : : : : : :
Db 110 SKESKSDSNLLIDSYKEIADENGADSAVLATKS 145
   : : : : : : : : : : : : : : : : : :

RESULT 6
O23304 PRELIMINARY; PRT; 487 AA.
AC O23304
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE SPE20-like kinase homolog (Kinase like protein).
GN AT4G14480.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Stiekema W., Murphy G., Wambutt R., Pohl T., Terry N.,
RA Kreis M., Kavanagh T., Entian K.D., Rieger M., James R.,
RA Puigdomenech P., Hatzopoulos P., Obermaier B., Duesterhoft A.,
RA Jones J., Palme K., Ansgore W., Delsen M., Bancroft I., Mewes H.W.,
RA Schueller C., Chalvatzis N.,
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z97336; CAB10227.1;
DR EMBL; AL161539; CAB78490.1;
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Transferase.
SQ SEQUENCE 487 AA; 54380 MW; 77D21D39D2FB4F20 CRC64;

Query Match 25.1%; Score 63.5; DB 10; Length 487;
Best Local Similarity 30.2%; Pred. No. 14;
Matches 13; Conservative 12; Mismatches 11; Indels 7; Gaps 1;
QY 9 APRDAGSQRPKRKEDNVLVESHEKSLGEANKADNVNLTAKSQ 51
   : : : : : : : : : : : : : : : : : :
Db 374 SPREDQSKDKEDDNTVITGYELGLSLNE-----EAKNQ 409
   : : : : : : : : : : : : : : : : : :

RESULT 7
Q98T05 PRELIMINARY; PRT; 975 AA.
AC Q98T05
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Myosin heavy chain (Fragment).
GN MYOHC-A3 GENE.
OS Notothenia coriiceps (black rockcod).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes;
OC Nototheniidae; Nototheniidae; Notothenia.
OX NCBI_TaxID=8208;
RN [1]
RP SEQUENCE FROM N.A.
RA Gauvre L., Ennion S., Ettelate C., Goldspink G.;
RT "Characterisation of red and white muscle myosin heavy chain gene

```

```

coding sequences from Antarctic and tropical fish.";
RL Comp. Biochem. Physiol. 127:575-588(2000).
DR EMBL; AJ243768; CAC27777.1;
DR HSSP; P03437; IHTM.
DR InterPro; IPR002928; Myosin_tail.
DR InterPro; IPR000533; Tropomyosin.
DR Pfam; PF01576; Myosin_tail; 1.
DR PRINTS; PR00194; TROPOMYOSIN.
FT NON_TER 1
SQ SEQUENCE 975 AA; 112313 MW; 2F7AD46A3419537F CRC64;

Query Match 24.9%; Score 63; DB 13; Length 975;
Best Local Similarity 45.5%; Pred. No. 34;
Matches 15; Conservative 7; Mismatches 9; Indels 2; Gaps 1;
QY 21 KEDNVLVESHEKSLG--EANKADNVNLTAKSQ 51
   : : : : : : : : : : : : : : : : : :
Db 34 KEKALQESHQOTLDDLQAEEDKVNLTAKTK 66
   : : : : : : : : : : : : : : : : : :

RESULT 8
P87344 PRELIMINARY; PRT; 1119 AA.
AC P87344
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myosin heavy chain (Fragment).
OS Theragra chalcogramma (Alaska pollock).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Theragra.
OX NCBI_TaxID=48550;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fast muscle;
RA Togashi M., Hirayama Y., Kakimura M., Watabe S., Ojima T., Nishita K.;
RT "cDNA cloning of Alaska polack fast skeletal muscle myosin heavy
chain.";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB000214; BAA19070.1;
DR HSSP; P13538; 2MYS.
DR InterPro; IPR002928; Myosin_tail.
DR InterPro; IPR000533; Tropomyosin.
DR Pfam; PF01576; Myosin_tail; 1.
DR PRINTS; PR00194; TROPOMYOSIN.
FT NON_TER 1
SQ SEQUENCE 1119 AA; 128626 MW; B8C5FECAE6F5B954 CRC64;

Query Match 24.9%; Score 63; DB 13; Length 1119;
Best Local Similarity 45.5%; Pred. No. 40;
Matches 15; Conservative 7; Mismatches 9; Indels 2; Gaps 1;
QY 21 KEDNVLVESHEKSLG--EANKADNVNLTAKSQ 51
   : : : : : : : : : : : : : : : : : :
Db 178 KEKALQESHQOTLDDLQAEEDKVNLTAKTK 210
   : : : : : : : : : : : : : : : : : :

RESULT 9
O93498 PRELIMINARY; PRT; 1287 AA.
AC O93498
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myosin heavy chain (Fragment).
OS Theragra chalcogramma (Alaska pollock).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Theragra.
OX NCBI_TaxID=48550;
RN [1]
RP SEQUENCE FROM N.A.

```



```

RC SEQUENCE FROM N.A.
RC TISSUE=Fast muscle;
RX MEDLINE=97176447; PubMed=9023993;
RA Imai J., Hirayama Y., Kikuchi K., Kakinuma M., Watabe S.;
RT "cDNA cloning of myosin heavy chain isoforms from carp fast skeletal
RT muscle and their gene expression associated with temperature
RT acclimation.";
RL J. Exp. Biol. 200:27-34(1997).
DR EMBL: D50475; BAA09068.1; -.
DR InterPro: IPR002928; Myosin_tail.
DR Pfam: PF01576; Myosin_tail; 1.
FT NON_TER
SQ SEQUENCE 1092 AA; 125885 MW; B6BABA3963BEEBA CRC64;

Query Match 23.7%; Score 60; DB 13; Length 1092;
Best Local Similarity 42.4%; Pred. No. 94;
Matches 14; Conservative 8; Mismatches 9; Indels 2; Gaps 1;

OY 21 KEDNVLVESHEKSLG--EANKADVNVLTAKSQ 51
DB 153 KEKALQEAHQQTLDLQAEEDKVNLTAKTK 185

RESULT 13
Q9DGD5 PRELIMINARY; PRT; 1930 AA.
AC Q9DGD5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Myosin heavy chain.
OS Pennahia argentata.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Sciaenidae; Pennahia.
OX NCBI_TaxID=118565;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fast muscle;
RA Yoon S., Kakinuma M., Hirayama Y., Yamamoto J., Watabe S.;
RT "cDNA cloning and characterization of the complete primary structure of
RT myosin heavy chain from white croaker fast skeletal muscle.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB039672; BAB12571.1; -.
DR HSSP: P13538; 2MYS.
DR InterPro: IPR000048; IQ_region.
DR InterPro: IPR001609; myosin_head.
DR InterPro: IPR004009; Myosin_N.
DR InterPro: IPR002928; Myosin_tail.
DR Pfam: PF00612; IQ; 1.
DR Pfam: PF00063; myosin_head; 1.
DR Pfam: PF02736; Myosin_N; 1.
DR Pfam: PF01576; Myosin_tail; 1.
DR PRINTS: PR00193; MYOSINHEAVY.
DR ProDom: PD000355; myosin_head; 1.
DR SMART: SM00015; IQ; 1.
DR SMART: SM00242; MYSC; 1.
DR PROSITE: PS50096; IQ; 1.
DR NCBI_TaxID=1930 AA; 221208 MW; C6219EB07CB4C5A1 CRC64;

Query Match 23.7%; Score 60; DB 13; Length 1930;
Best Local Similarity 42.4%; Pred. No. 1.8e+02;
Matches 14; Conservative 8; Mismatches 9; Indels 2; Gaps 1;

OY 21 KEDNVLVESHEKSLG--EANKADVNVLTAKSQ 51
DB 989 KEKALQEAHQQTLDLQAEEDKVNLTAKTK 1021

RESULT 14
Q910C5 PRELIMINARY; PRT; 1931 AA.
ID Q910C5
RC TISSUE=Fast muscle;
RX MEDLINE=97352533; PubMed=9208928;
RA Hirayama Y., Watabe S.;
RT "Structural differences in the crossbridge head of temperature-
RT associated myosin subfragment-1 isoforms from carp fast skeletal
RT muscle.";
RL Eur. J. Biochem. 246:380-387(1997).
DR EMBL: D89991; BAA22068.1; -.
DR HSSP: P13538; 2MYS.
DR InterPro: IPR000048; IQ_region.
DR InterPro: IPR001609; myosin_head.
DR InterPro: IPR004009; Myosin_N.

```

```

AC Q910C5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Chick atrial myosin heavy chain.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Oana S., Machida S., Furutani Y., Hiratsuka E., Momma K., Takao A.,
RA Matsuoka R.;
RT "Characterization and expression pattern of atrial myosin heavy chain
RT gene in developing chick.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB004801; BAB47399.1; -.
DR InterPro: IPR000048; IQ_region.
DR InterPro: IPR001609; myosin_head.
DR InterPro: IPR004009; Myosin_N.
DR InterPro: IPR002928; Myosin_tail.
DR InterPro: IPR002017; Spectrin.
DR InterPro: IPR000533; Tropomyosin.
DR Pfam: PF00612; IQ; 2.
DR Pfam: PF00063; myosin_head; 1.
DR Pfam: PF02736; Myosin_N; 1.
DR Pfam: PF01576; Myosin_tail; 1.
DR PRINTS: PR00193; MYOSINHEAVY.
DR ProDom: PD000355; myosin_head; 1.
DR SMART: SM00015; IQ; 1.
DR SMART: SM00242; MYSC; 1.
DR PROSITE: PS50096; IQ; 1.
DR NCBI_TaxID=1931 AA; 221802 MW; EB57D688E03397D2 CRC64;

Query Match 23.7%; Score 60; DB 13; Length 1931;
Best Local Similarity 42.4%; Pred. No. 1.8e+02;
Matches 14; Conservative 7; Mismatches 10; Indels 2; Gaps 1;

OY 21 KEDNVLVESHEKSLG--EANKADVNVLTAKSQ 51
DB 989 KEKILQESHQQLDLDLQAEEDKVNLTAKAKG 1021

RESULT 15
O42352 PRELIMINARY; PRT; 1931 AA.
AC O42352;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Myosin heavy chain.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fast muscle;
RX MEDLINE=97352533; PubMed=9208928;
RA Hirayama Y., Watabe S.;
RT "Structural differences in the crossbridge head of temperature-
RT associated myosin subfragment-1 isoforms from carp fast skeletal
RT muscle.";
RL Eur. J. Biochem. 246:380-387(1997).
DR EMBL: D89991; BAA22068.1; -.
DR HSSP: P13538; 2MYS.
DR InterPro: IPR000048; IQ_region.
DR InterPro: IPR001609; myosin_head.
DR InterPro: IPR004009; Myosin_N.

```

Search completed: October 9, 2003, 08:13:33
Job time : 47.6716 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2003, 08:08:57 ; Search time 12.9403 Seconds
(without alignments)
166.755 Million cell updates/sec

Title: US-09-928-048A-5
Perfect score: 253
Sequence: 1 FVALGAPLAPRDAGSORPRK.....KSLGEANKADYVLTAKSQ 51

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	248	98.0	51	3	US-09-044-536A-7
2	248	98.0	51	4	US-10-002-818-3
3	248	98.0	83	4	US-10-002-818-2
4	248	98.0	84	1	US-07-863-014-2
5	248	98.0	84	1	US-08-332-453-2
6	248	98.0	84	1	US-08-689-190-2
7	248	98.0	84	2	US-08-835-231-9
8	248	98.0	84	2	US-08-805-918-3
9	248	98.0	84	3	US-09-044-536A-36
10	248	98.0	84	3	US-09-108-861-9
11	248	98.0	84	4	US-10-002-818-1
12	248	98.0	84	5	PCT-US95-15800-25
13	243	96.0	84	2	US-08-142-551B-1
14	243	96.0	84	2	US-08-411-726-1
15	238	94.1	84	1	US-07-707-114-1
16	237	93.7	50	2	US-08-142-551B-119
17	209	82.6	78	2	US-08-733-446-1
18	209	82.6	79	2	US-08-733-446-2
19	209	82.6	80	2	US-08-733-446-3
20	209	82.6	81	2	US-08-733-446-4
21	209	82.6	84	2	US-08-733-446-5
22	199	78.7	84	1	US-07-773-098-1
23	199	78.7	84	1	US-07-773-098-2
24	199	78.7	84	1	US-07-773-098-7
25	199	78.7	84	1	US-07-773-098-8
26	199	78.7	84	1	US-07-773-098-9
27	199	78.7	84	1	US-07-773-098-10

28	194	76.7	84	1	US-07-776-272-14	Sequence 14, Appl
29	59	23.3	419	4	US-09-252-991A-29836	Sequence 29836, A
30	58	22.9	1120	4	US-09-147-404-1	Sequence 1, Appl1
31	56	22.1	237	4	US-09-252-991A-19408	Sequence 19408, A
32	55	21.7	1886	4	US-08-938-105-3	Sequence 3, Appl1
33	54.5	21.5	740	4	US-09-252-991A-21575	Sequence 21575, A
34	54.5	21.5	801	4	US-09-134-001C-5584	Sequence 5584, Ap
35	52.5	20.8	185	3	US-09-154-083-14	Sequence 14, Appl
36	52	20.6	133	3	US-08-961-784-188	Sequence 188, App
37	52	20.6	133	4	US-09-536-784-188	Sequence 188, App
38	52	20.6	287	1	US-08-624-125-17	Sequence 17, Appl
39	52	20.6	287	1	US-08-937-155-17	Sequence 17, Appl
40	51	20.2	135	4	US-09-252-991A-19405	Sequence 19405, A
41	51	20.2	212	4	US-09-369-247-88	Sequence 88, Appl
42	51	20.2	337	4	US-09-252-991A-16886	Sequence 16886, A
43	51	20.2	497	4	US-09-252-991A-23620	Sequence 23620, A
44	51	20.2	706	1	US-08-339-152A-29	Sequence 29, Appl
45	51	20.2	706	2	US-08-007-999B-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-09-044-536A-7
; Sequence 7, Application US/09044536A
; Patent No. 6025467
; GENERAL INFORMATION:
; APPLICANT: FUKUDA, Tsunehiko
; APPLICANT: NAKAGAWA, Shizue
; APPLICANT: HABASHITA, Junko
; APPLICANT: TAKETOMI, Shigehisa
; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES AND THEIR USE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/044,536A
; FILING DATE: 19-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/662,871
; FILING DATE: 12-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: CONLIN, David G
; REGISTRATION NUMBER: 27,026
; REFERENCE/DOCKET NUMBER: 46509-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 51 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: partial peptide
; LOCATION: 1..51
; US-09-044-536A-7

Query Match 98.0%; Score 248; DB 3; Length 51;
Best Local Similarity 98.0%; Pred. No. 6.3e-28;

Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSQPRKEDNVLSHEKSLGEANKADNVNLTAKSQ 51
|||||
Db 1 FVALGAPLAPRDAGSQPRKEDNVLSHEKSLGEANKADNVNLTAKSQ 51
|||||

RESULT 2

US-10-002-818-3
; Sequence 3, Application US/10002818
; Patent No. 6524788
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas L.
; TITLE OF INVENTION: Methods for Monitoring Therapeutic Suppression of Parathyroid Hormone
; TITLE OF INVENTION: Renal Patients Having Secondary Hyperparathyroidism
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/002,818
; CURRENT FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Microsoft Word 2000 - ASCII format
; SEQ ID NO 3
; LENGTH: 51
; TYPE: PRT
; ORGANISM: human parathyroid hormone peptide fragment
US-10-002-818-3

Query Match 98.0%; Score 248; DB 4; Length 51;
Best Local Similarity 98.0%; Pred. No. 6.3e-28;
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSQPRKEDNVLSHEKSLGEANKADNVNLTAKSQ 51
|||||
Db 1 FVALGAPLAPRDAGSQPRKEDNVLSHEKSLGEANKADNVNLTAKSQ 51
|||||

RESULT 3

US-10-002-818-2
; Sequence 2, Application US/10002818
; Patent No. 6524788
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas L.
; TITLE OF INVENTION: Methods for Monitoring Therapeutic Suppression of Parathyroid Hormone
; TITLE OF INVENTION: Renal Patients Having Secondary Hyperparathyroidism
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/002,818
; CURRENT FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Microsoft Word 2000 - ASCII format
; SEQ ID NO 2
; LENGTH: 83
; TYPE: PRT
; ORGANISM: human parathyroid hormone peptide fragment
US-10-002-818-2

Query Match 98.0%; Score 248; DB 4; Length 83;
Best Local Similarity 98.0%; Pred. No. 1.2e-27;
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSQPRKEDNVLSHEKSLGEANKADNVNLTAKSQ 51
|||||
Db 33 FVALGAPLAPRDAGSQPRKEDNVLSHEKSLGEANKADNVNLTAKSQ 83
|||||

RESULT 4

US-07-863-014-2
; Sequence 2, Application US/07863014
; Patent No. 5382658
; GENERAL INFORMATION:
; APPLICANT: KRONIS, K. Anne
; APPLICANT: BOZZATO, Richard P.
; TITLE OF INVENTION: STABILITY-ENHANCED VARIANTS OF
; TITLE OF INVENTION: PARATHYROID HORMONE
; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/863,014
; FILING DATE: 19920403
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16777/163 ALLE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-863-014-2

Query Match 98.0%; Score 248; DB 1; Length 84;
Best Local Similarity 98.0%; Pred. No. 1.2e-27;
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSQPRKEDNVLSHEKSLGEANKADNVNLTAKSQ 51
|||||
Db 34 FVALGAPLAPRDAGSQPRKEDNVLSHEKSLGEANKADNVNLTAKSQ 84
|||||

RESULT 5

US-08-332-453-2
; Sequence 2, Application US/08332453
; Patent No. 5599792
; GENERAL INFORMATION:
; APPLICANT: KRONIS, K. Anne
; APPLICANT: BOZZATO, Richard P.
; TITLE OF INVENTION: BONE-STIMULATING, NON-VASOACTIVE
; TITLE OF INVENTION: PARATHYROID HORMONE VARIANTS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,453
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/900,680
; FILING DATE: 19-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 16777/182 ALLE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-332-453-2

Query Match 98.0%; Score 248; DB 1; Length 84;
Best Local Similarity 98.0%; Pred. No. 1.2e-27;
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSORPKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 51
Db 34 FVALGAPLAPRDAGSORPKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 84

RESULT 6

US-08-689-190-2
Sequence 2, Application US/08689190
Patent No. 5714349

GENERAL INFORMATION:
APPLICANT: FUKUDA, Tsunehiko
APPLICANT: OSHIKA, Yuri
APPLICANT: YAMADA, Takao
TITLE OF INVENTION: SYNTHETIC GENE CODING FOR HUMAN
TITLE OF INVENTION: PARATHYROID HORMONE
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
STREET: 130 Water Street
CITY: Boston
STATE: Massachusetts
COUNTRY: US
ZIP: 02109
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/689,190
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/006,197
FILING DATE:
APPLICATION NUMBER: US/08/016,171
FILING DATE:
APPLICATION NUMBER: US/07/765,371
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, Gregory D
REGISTRATION NUMBER: 30,901
REFERENCE/DOCKET NUMBER: 41,288
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-689-190-2

Query Match

98.0%; Score 248; DB 1; Length 84;

Best Local Similarity 98.0%; Pred. No. 1.2e-27;
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSORPKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 51
Db 34 FVALGAPLAPRDAGSORPKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 84

RESULT 7

US-08-835-231-9
Sequence 9, Application US/08835231
Patent No. 5861284

GENERAL INFORMATION:
APPLICANT: NISHIMURA, Osamu
APPLICANT: KURIYAMA, Masato
APPLICANT: KOYAMA, No. 5861284uyuki
APPLICANT: FUKUDA, Tsunehiko
TITLE OF INVENTION: METHOD FOR PRODUCING A BIOLOGICALLY
TITLE OF INVENTION: ACTIVE RECOMBINANT CYSTEINE-FREE
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/835,231
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,709
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: 07/838,857
FILING DATE: 18-FEB-1992
APPLICATION NUMBER: JP 024841
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: JP 0271438
FILING DATE: 18-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 41614-FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STRE

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-835-231-9

Query Match 98.0%; Score 248; DB 2; Length 84;
Best Local Similarity 98.0%; Pred. No. 1.2e-27;
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSORPKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 51
Db 34 FVALGAPLAPRDAGSORPKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 84

```

RESULT 8
US-08-805-918-3
; Sequence 3, Application US/0805918
; Patent No. 5885821
; GENERAL INFORMATION:
; APPLICANT: MAGOTA, KOJI
; APPLICANT: MASUDA, TOYOFUMI
; APPLICANT: SUZUKI, YUJI
; APPLICANT: YABUTA, MASAYUKI
; TITLE OF INVENTION: PROCESS FOR PRODUCTION OF SECRETORY KEX2
; TITLE OF INVENTION: DERIVATIVES
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/805,918
; FILING DATE: 04-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-073217
; FILING DATE: 04-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8-352580
; FILING DATE: 16-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M.
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 001560-295
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-805-918-3

Query Match 98.08; Score 248; DB 2; Length 84;
Best Local Similarity 98.08; Pred. No. 1.2e-27;
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVALGAPLRDAGSQPRKKEDNVLVESKSLGEANKADVNVLTAKSQ 51
|||||
Db 34 FVALGAPLRDAGSQPRKKEDNVLVESKSLGEANKADVNVLTAKSQ 84
|||||

RESULT 9
US-09-044-536A-36
; Sequence 36, Application US/09044536A
; Patent No. 6025467
; GENERAL INFORMATION:
; APPLICANT: FUKUDA, Tsunehiko
; APPLICANT: NAKAGAWA, Shizue
; APPLICANT: HAKASHITA, Junko
; APPLICANT: TAKETOMI, Shigehisa
; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES AND THEIR USE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/044,536A
; FILING DATE: 19-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/662,871
; FILING DATE: 12-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: CONLIN, David G
; REGISTRATION NUMBER: 27,026
; REFERENCE/DOCKET NUMBER: 46509-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 10
; OTHER INFORMATION: Xaa-acidic amino acid;
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: Xaa-hydrophobic alpha amino acid, basic
; OTHER INFORMATION: amino acid;
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 12
; OTHER INFORMATION: Xaa-Gly, Ala, Ser, Lys, Orn;
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 13
; OTHER INFORMATION: Xaa= basic amino acid;
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 14
; OTHER INFORMATION: Xaa= basic amino acid;
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 15
; OTHER INFORMATION: Xaa= aliphatic neutral amino acid, basic
; OTHER INFORMATION: amino acid;
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 16,17
; OTHER INFORMATION: Xaa= non-charged hydrophilic amino acid-
; OTHER INFORMATION: basic amino acid;
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 19
; OTHER INFORMATION: Xaa= acidic amino acid, basic amino acid;
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 21
; OTHER INFORMATION: Xaa= aliphatic neutral amino acid, basic
; OTHER INFORMATION: amino acid;
; FEATURE:
; NAME/KEY: Modified-site

```

LOCATION: 26
OTHER INFORMATION: Xaa= basic amino acid;
FEATURE:
NAME/KEY: Modified-site
LOCATION: 27
OTHER INFORMATION: Xaa= non-charged hydrophilic amino acid,
OTHER INFORMATION: basic amino acid;
FEATURE:
NAME/KEY: Modified-site
LOCATION: 30
OTHER INFORMATION: Xaa= acidic amino acid, aliphatic neutral
OTHER INFORMATION: amino acid;
US-09-044-536A-36

Query Match 98.0%; Score 248; DB 3; Length 84;
Best Local Similarity 98.0%; Pred. No. 1.2e-27;
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSQRPKKEDNVLSHESKSLGEAKADNVNLTAKSQ 51
|||||
DB 34 FVALGAPLAPRDAGSQRPKKEDNVLSHESKSLGEAKADNVNLTAKSQ 84
|||||

RESULT 10

US-09-108-661-9
Sequence 9, Application US/09108661
Patent No. 6287806

GENERAL INFORMATION:

APPLICANT: NISHIMURA, Osamu
APPLICANT: KURIYAMA, Masato
APPLICANT: KOYAMA, No. 6287806uyuk1
APPLICANT: FUKUDA, Tsunehiko
TITLE OF INVENTION: METHOD FOR PRODUCING A BIOLOGICALLY
TITLE OF INVENTION: ACTIVE RECOMBINANT CYSTEINE-FREE
NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/108,661
FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,709
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: 07/838,857
FILING DATE: 18-FEB-1992
APPLICATION NUMBER: JP 024841
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: JP 0271438
FILING DATE: 18-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 41614-FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
TELEX: 200291 STRE

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-09-108-661-9

Query Match 98.0%; Score 248; DB 3; Length 84;
Best Local Similarity 98.0%; Pred. No. 1.2e-27;
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSQRPKKEDNVLSHESKSLGEAKADNVNLTAKSQ 51
|||||
DB 34 FVALGAPLAPRDAGSQRPKKEDNVLSHESKSLGEAKADNVNLTAKSQ 84
|||||

RESULT 11

US-10-002-818-1
Sequence 1, Application US/10002818
Patent No. 6524788

GENERAL INFORMATION:

APPLICANT: Cantor, Thomas L.
TITLE OF INVENTION: Methods for Monitoring Therapeutic Suppression of Parathyroidism
TITLE OF INVENTION: Renal Patients Having Secondary Hyperparathyroidism
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/002,818
CURRENT FILING DATE: 2001-11-02
NUMBER OF SEQ ID NOS: 3

SOFTWARE: Microsoft Word 2000 - ASCII format
SEQ ID NO 1
LENGTH: 84

TYPE: PRT

ORGANISM: human parathyroid hormone peptide fragment
US-10-002-818-1

Query Match 98.0%; Score 248; DB 4; Length 84;
Best Local Similarity 98.0%; Pred. No. 1.2e-27;
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSQRPKKEDNVLSHESKSLGEAKADNVNLTAKSQ 51
|||||
DB 34 FVALGAPLAPRDAGSQRPKKEDNVLSHESKSLGEAKADNVNLTAKSQ 84
|||||

RESULT 12

PCT-US95-15800-25
Sequence 25, Application PC/TUS9515800
GENERAL INFORMATION:

APPLICANT: Blonbraska, Inc.
TITLE OF INVENTION: PRODUCTION OF PEPTIDES USING
TITLE OF INVENTION: RECOMBINANT FUSION PROTEIN CONSTRUCTS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 3100 Norwest Center, 90 S. 7th Street
CITY: Minneapolis
STATE: MN
COUNTRY: U.S.A.
ZIP: 55402

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/15800
FILING DATE: 07-DEC-1995

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,530
FILING DATE: 07-DEC-1994
ATTORNEY/AGENT INFORMATION:

NAME: Carter, Charles G
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.45USWO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/332-5300
TELEFAX: 612/332-9081
TELEX:

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:
LENGTH: 84 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
PCT-0595-15800-25

Query Match 98.0%; Score 248; DB 5; Length 84;
Best Local Similarity 98.0%; Pred. No. 1.2e-27;
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSQRPKKEDNVLVESHSKSLGEANKADYVNLTKAKSQ 51
|||||
DB 34 FVALGAPLAPRDAGSQRPKKEDNVLVESHSKSLGEANKADYVNLTKAKSQ 84
|||||

RESULT 13

US-08-142-551B-1

; Sequence 1, Application US/08142551B

; Patent No. 5814603

; GENERAL INFORMATION:

; APPLICANT: Oldenburg, Kevin R.

; APPLICANT: Selick, Harold E.

; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND

; TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME

; NUMBER OF SEQUENCES: 132

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Burns, Doane, Svecker & Mathis

; STREET: 699 Prince Street

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: US

; ZIP: 22313

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/142,551B

; FILING DATE: 25-OCT-1993

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/077,296

; FILING DATE: 14-JUN-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/898,219

; FILING DATE: 12-JUN-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/965,677

; FILING DATE: 22-OCT-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Swiss, Gerald F.

; REGISTRATION NUMBER: 30,113

; REFERENCE/DOCKET NUMBER: 000324-010

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 854-7400

; TELEFAX: (415) 854-8275

; INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 84 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
FEATURE:

NAME/KEY: Protein

LOCATION: 1..84

OTHER INFORMATION: /note= "84 amino acid PTH"

US-08-142-551B-1

Query Match

Best Local Similarity 96.0%; Score 243; DB 2; Length 84;

Matches 49; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSQRPKKEDNVLVESHSKSLGEANKADYVNLTKAKSQ 51
|||||

DB 34 FVALGAPLAPRDAGSQRPKKEDNVLVESHSKSLGEANKADYVNLTKAKSQ 84
|||||

RESULT 14

US-08-411-726-1

; Sequence 1, Application US/08411726

; Patent No. 5880093

; GENERAL INFORMATION:

; APPLICANT: BAGNOLI, Franco

; TITLE OF INVENTION: Use of Parathormone, Its Biologically

; TITLE OF INVENTION: Active Fragments and Correlated Peptides, for The Prep

; TITLE OF INVENTION: Pharmaceutical Compositions Useful for The Treatment o

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Kenyon & Kenyon

; STREET: 1 Broadway

; CITY: New York

; STATE: NY

; COUNTRY: US

; ZIP: 10004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS 6.2

; SOFTWARE: WordPerfect 6.1 for Windows

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/411,726

; FILING DATE: 05-APR-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/EP93/02755

; FILING DATE: 08-OCT-1993

; APPLICATION NUMBER: MI-92A002331

; FILING DATE: 09-OCT-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: PALMESE, Maria Luisa

; REGISTRATION NUMBER: 34,402

; REFERENCE/DOCKET NUMBER: 2111/1300

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-425-7200

; TELEFAX: 212-425-5288

; INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 84 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-411-726-1

Query Match

Best Local Similarity 96.0%; Score 243; DB 2; Length 84;

Matches 49; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSQRPKKEDNVLVESHSKSLGEANKADYVNLTKAKSQ 51
|||||

DB 34 FVALGAPLAPRDAGSQRPKKEDNVLVESHSKSLGEANKADYVNLTKAKSQ 84
|||||

RESULT 15
 US-07-707-114-1
 ; Sequence 1, Application US/07707114
 ; Patent No. 5208041
 ; GENERAL INFORMATION:
 ; APPLICANT: SINDREY, Dennis R.
 ; TITLE OF INVENTION: ESSENTIALLY PURE HUMAN PARATHYROID
 ; TITLE OF INVENTION: HORMONE
 ; NUMBER OF SEQUENCES: 1
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 1800 Diagonal Road, Suite 500
 ; CITY: Alexandria
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22313-0299
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/707,114
 ; FILING DATE: 19910523
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BENT, Stephen A.
 ; REGISTRATION NUMBER: 29,768
 ; REFERENCE/DOCKET NUMBER: 16777/147 ALLE
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703)836-9300
 ; TELEFAX: (703)683-4109
 ; TELEX: 899149
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 84 amino acids
 ; TYPE: AMINO ACID
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; ORIGINAL SOURCE:
 ; ORGANISM: homo sapiens
 ; IMMEDIATE SOURCE:
 ; CLONE: hPTH
 ; US-07-707-114-1

Query Match 94.1%; Score 238; DB 1; Length 84;
 Best Local Similarity 94.1%; Pred. No. 3,1e-26;
 Matches 48; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSQPRKEDNVLVESKSLGKANKADYVLTAKSQ 51
 DB 34 FVALGAPLAPRDAGSQPRKEDNVLVESKSLGKANKADYVLTAKSQ 84

Search completed: October 9, 2003, 08:15:10
 Job time : 12.9403 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2003, 08:10:52; Search time 95.1493 Seconds
(without alignments)
86.365 Million cell updates/sec

Title: US-09-928-048A-5
Perfect score: 253
Sequence: 1 FVALGAPLAPRDAGSORPRK.....KSLGEANKADVNVLTAKSQ 51

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 600653 seqs, 161128416 residues

Total number of hits satisfying chosen parameters: 600653

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published_Applications_AA:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	253	100.0	51	10	US-09-928-047B-3
2	253	100.0	51	12	US-09-928-048A-5
3	253	100.0	57	10	US-09-928-047B-8
4	253	100.0	78	10	US-09-928-047B-4
5	253	100.0	82	10	US-09-928-047B-2
6	253	100.0	83	10	US-09-928-047B-1
7	253	100.0	84	12	US-09-928-048A-3
8	253	100.0	84	12	US-09-928-047B-5
9	253	100.0	84	12	US-09-928-048A-3
10	253	100.0	84	12	US-09-928-048A-3
11	248	98.0	78	11	US-09-843-221A-12
12	248	98.0	84	9	US-09-169-786-1
13	248	98.0	84	11	US-09-843-221A-10
14	248	98.0	84	11	US-09-898-398-1
15	248	98.0	115	15	US-10-157-031-50

16	247	97.6	50	10	US-09-928-047B-7	Sequence 7, Appl1
17	247	97.6	50	12	US-09-928-048A-7	Sequence 7, Appl1
18	206	81.4	84	15	US-10-215-770-3	Sequence 3, Appl1
19	199	78.7	84	9	US-09-879-257A-49	Sequence 49, Appl1
20	199	78.7	84	15	US-10-215-770-4	Sequence 4, Appl1
21	194	76.7	84	15	US-10-215-770-2	Sequence 2, Appl1
22	164	64.8	84	11	US-09-843-221A-11	Sequence 11, Appl1
23	160	63.2	84	15	US-10-215-770-5	Sequence 5, Appl1
24	95	37.5	20	12	US-09-928-048A-8	Sequence 8, Appl1
25	68.5	27.1	88	15	US-10-215-770-6	Sequence 6, Appl1
26	61	24.1	557	9	US-09-815-242-12165	Sequence 12165, A
27	61	24.1	563	9	US-09-815-242-5464	Sequence 5464, Ap
28	59	23.3	566	16	US-10-282-287-4	Sequence 4, Appl1
29	59	23.3	557	9	US-09-815-242-12804	Sequence 12804, A
30	57	22.5	238	10	US-09-323-998D-41	Sequence 41, Appl1
31	55.5	21.9	46	9	US-09-864-761-34138	Sequence 34138, A
32	55	21.7	44	11	US-09-843-221A-13	Sequence 13, Appl1
33	55	21.7	1157	10	US-09-935-291A-12	Sequence 12, Appl1
34	55	21.7	1518	10	US-09-801-368-152	Sequence 152, App
35	54	21.3	1033	11	US-09-820-843A-75	Sequence 75, Appl1
36	54	21.3	1075	15	US-10-156-761-10208	Sequence 10208, A
37	52.5	20.8	521	12	US-10-168-651-26	Sequence 26, Appl1
38	52.5	20.8	552	15	US-10-225-567A-430	Sequence 430, App
39	52	20.6	133	9	US-09-765-272-188	Sequence 188, App
40	52	20.6	241	15	US-10-278-173-78	Sequence 78, Appl1
41	52	20.6	287	10	US-09-323-998D-17	Sequence 17, Appl1
42	52	20.6	399	12	US-09-769-744A-94	Sequence 94, Appl1
43	52	20.6	682	9	US-09-815-242-11214	Sequence 11214, A
44	51.5	20.4	425	15	US-10-128-714-3260	Sequence 3260, Ap
45	51.5	20.4	425	15	US-10-128-714-8260	Sequence 8260, Ap

ALIGNMENTS

RESULT 1
US-09-928-047B-3
; Sequence 3, Application US/09928047B
; Patent No. US20020160945A1
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas
; TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
; TITLE OF INVENTION: ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
; FILE REFERENCE: 53221-20002.00
; CURRENT APPLICATION NUMBER: US/09/928,047B
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/224,446
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-047B-3

Query Match 100.0%; Score 253; DB 10; Length 51;
Best Local Similarity 100.0%; Pred. No. 7.8e-26;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FVALGAPLAPRDAGSORPRKEDNVLSVESKSLGEANKADVNVLTAKSQ 51
DB 1 FVALGAPLAPRDAGSORPRKEDNVLSVESKSLGEANKADVNVLTAKSQ 51

RESULT 2
US-09-928-048A-5
; Sequence 5, Application US/09928048A
; Publication No. US20030138858A1
; GENERAL INFORMATION:
; APPLICANT: Scantibodies Laboratory, Inc.
; APPLICANT: Cantor, Thomas L.
; TITLE OF INVENTION: METHODS AND DEVICES FOR DIRECT

;; TITLE OF INVENTION: DETERMINATION OF CYCLASE INHIBITING PARATHYROID HORMONE
;; FILE REFERENCE: 53221-20015.00
;; CURRENT APPLICATION NUMBER: US/09/928,048A
;; NUMBER OF SEQ ID NOS: 8
;; SOFTWARE: FastSeq for Windows Version 4.0

;; SEQ ID NO 5

;; LENGTH: 51

;; TYPE: PRT

;; ORGANISM: Homo sapiens

US-09-928-048A-5

Query Match 100.0%; Score 253; DB 12; Length 51;
Best Local Similarity 100.0%; Pred. No. 7.8e-26;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVALGAPLAPRDAGSQRPKKEDNVLVESHEKSLGEANKADVNVLTAKSQ 51

Db 1 FVALGAPLAPRDAGSQRPKKEDNVLVESHEKSLGEANKADVNVLTAKSQ 51

RESULT 3

US-09-928-047B-8

;; Sequence 8, Application US/09928047B

;; Patent No. US20020160945A1

;; GENERAL INFORMATION:

;; APPLICANT: Cantor, Thomas

;; TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE

;; FILE REFERENCE: 53221-20002.00

;; CURRENT APPLICATION NUMBER: US/09/928,047B

;; CURRENT FILING DATE: 2001-08-10

;; PRIOR APPLICATION NUMBER: US 60/224,446

;; PRIOR FILING DATE: 2000-08-10

;; NUMBER OF SEQ ID NOS: 8

;; SOFTWARE: FastSeq for Windows Version 4.0

;; SEQ ID NO 8

;; LENGTH: 57

;; TYPE: PRT

;; ORGANISM: Homo sapiens

US-09-928-047B-8

Query Match 100.0%; Score 253; DB 10; Length 57;
Best Local Similarity 100.0%; Pred. No. 8.9e-26;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVALGAPLAPRDAGSQRPKKEDNVLVESHEKSLGEANKADVNVLTAKSQ 51

Db 7 FVALGAPLAPRDAGSQRPKKEDNVLVESHEKSLGEANKADVNVLTAKSQ 57

RESULT 4

US-09-928-047B-4

;; Sequence 4, Application US/09928047B

;; Patent No. US20020160945A1

;; GENERAL INFORMATION:

;; APPLICANT: Cantor, Thomas

;; TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE

;; FILE REFERENCE: 53221-20002.00

;; CURRENT APPLICATION NUMBER: US/09/928,047B

;; CURRENT FILING DATE: 2001-08-10

;; PRIOR APPLICATION NUMBER: US 60/224,446

;; PRIOR FILING DATE: 2000-08-10

;; NUMBER OF SEQ ID NOS: 8

;; SOFTWARE: FastSeq for Windows Version 4.0

;; SEQ ID NO 4

;; LENGTH: 78

;; TYPE: PRT

;; ORGANISM: Homo sapiens

US-09-928-047B-4

Query Match 100.0%; Score 253; DB 10; Length 78;

Best Local Similarity 100.0%; Pred. No. 1.3e-25;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVALGAPLAPRDAGSQRPKKEDNVLVESHEKSLGEANKADVNVLTAKSQ 51

Db 28 FVALGAPLAPRDAGSQRPKKEDNVLVESHEKSLGEANKADVNVLTAKSQ 78

RESULT 5

US-09-928-047B-2

;; Sequence 2, Application US/09928047B

;; Patent No. US20020160945A1

;; GENERAL INFORMATION:

;; APPLICANT: Cantor, Thomas

;; TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE

;; FILE REFERENCE: 53221-20002.00

;; CURRENT APPLICATION NUMBER: US/09/928,047B

;; CURRENT FILING DATE: 2001-08-10

;; PRIOR APPLICATION NUMBER: US 60/224,446

;; PRIOR FILING DATE: 2000-08-10

;; NUMBER OF SEQ ID NOS: 8

;; SOFTWARE: FastSeq for Windows Version 4.0

;; SEQ ID NO 2

;; LENGTH: 82

;; TYPE: PRT

;; ORGANISM: Homo sapiens

US-09-928-047B-2

Query Match 100.0%; Score 253; DB 10; Length 82;

Best Local Similarity 100.0%; Pred. No. 1.4e-25;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVALGAPLAPRDAGSQRPKKEDNVLVESHEKSLGEANKADVNVLTAKSQ 51

Db 32 FVALGAPLAPRDAGSQRPKKEDNVLVESHEKSLGEANKADVNVLTAKSQ 82

RESULT 6

US-09-928-047B-1

;; Sequence 1, Application US/09928047B

;; Patent No. US20020160945A1

;; GENERAL INFORMATION:

;; APPLICANT: Cantor, Thomas

;; TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE

;; FILE REFERENCE: 53221-20002.00

;; CURRENT APPLICATION NUMBER: US/09/928,047B

;; CURRENT FILING DATE: 2001-08-10

;; PRIOR APPLICATION NUMBER: US 60/224,446

;; PRIOR FILING DATE: 2000-08-10

;; NUMBER OF SEQ ID NOS: 8

;; SOFTWARE: FastSeq for Windows Version 4.0

;; SEQ ID NO 1

;; LENGTH: 83

;; TYPE: PRT

;; ORGANISM: Homo sapiens

US-09-928-047B-1

Query Match 100.0%; Score 253; DB 10; Length 83;

Best Local Similarity 100.0%; Pred. No. 1.4e-25;

Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FVALGAPLAPRDAGSQRPKKEDNVLVESHEKSLGEANKADVNVLTAKSQ 51

Db 33 FVALGAPLAPRDAGSQRPKKEDNVLVESHEKSLGEANKADVNVLTAKSQ 83

RESULT 7

US-09-928-048A-4

;; Sequence 4, Application US/09928048A

;; Publication No. US20030138858A1

;; GENERAL INFORMATION:


```
; APPLICANT: Scantibodies Laboratory, Inc.
; APPLICANT: Cantor, Thomas L.
; TITLE OF INVENTION: METHODS AND DEVICES FOR DIRECT
; TITLE OF INVENTION: DETERMINATION OF CYCLASE INHIBITING PARATHYROID HORMONE
; FILE REFERENCE: 53221-20015.00
; CURRENT APPLICATION NUMBER: US/09/928,048A
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-048A-4

Query Match      100.0%; Score 253; DB 12; Length 83;
Best Local Similarity 100.0%; Pred. No. 1.4e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSORPKKEDNVLSHEKSLGKANKADVNVLTKAKSQ 51
Db 33 FVALGAPLAPRDAGSORPKKEDNVLSHEKSLGKANKADVNVLTKAKSQ 83

RESULT 8
US-09-928-047B-5
; Sequence 5, Application US/09928047B
; Patent No. US20020160945A1
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas
; TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
; TITLE OF INVENTION: ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
; FILE REFERENCE: 53221-20002.00
; CURRENT APPLICATION NUMBER: US/09/928,047B
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/224,446
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-047B-5

Query Match      100.0%; Score 253; DB 10; Length 84;
Best Local Similarity 100.0%; Pred. No. 1.4e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSORPKKEDNVLSHEKSLGKANKADVNVLTKAKSQ 51
Db 34 FVALGAPLAPRDAGSORPKKEDNVLSHEKSLGKANKADVNVLTKAKSQ 84

RESULT 9
US-09-928-048A-3
; Sequence 3, Application US/09928048A
; Publication No. US20030138658A1
; GENERAL INFORMATION:
; APPLICANT: Scantibodies Laboratory, Inc.
; APPLICANT: Cantor, Thomas L.
; TITLE OF INVENTION: METHODS AND DEVICES FOR DIRECT
; TITLE OF INVENTION: DETERMINATION OF CYCLASE INHIBITING PARATHYROID HORMONE
; FILE REFERENCE: 53221-20015.00
; CURRENT APPLICATION NUMBER: US/09/928,048A
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-048A-3
```

```
Query Match      100.0%; Score 253; DB 12; Length 84;
Best Local Similarity 100.0%; Pred. No. 1.4e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSORPKKEDNVLSHEKSLGKANKADVNVLTKAKSQ 51
Db 34 FVALGAPLAPRDAGSORPKKEDNVLSHEKSLGKANKADVNVLTKAKSQ 84

RESULT 10
US-10-215-770-1
; Sequence 1, Application US/10215770
; Publication No. US20030087822A1
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas L.
; TITLE OF INVENTION: PARATHYROID HORMONE ANTAGONISTS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 53221-20002.20
; CURRENT APPLICATION NUMBER: US/10/215,770
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US 60/224,446
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US 60/224,447
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-215-770-1

Query Match      100.0%; Score 253; DB 15; Length 84;
Best Local Similarity 100.0%; Pred. No. 1.4e-25;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FVALGAPLAPRDAGSORPKKEDNVLSHEKSLGKANKADVNVLTKAKSQ 51
Db 34 FVALGAPLAPRDAGSORPKKEDNVLSHEKSLGKANKADVNVLTKAKSQ 84

RESULT 11
US-09-843-221A-12
; Sequence 12, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENIUK, PAUL
; APPLICANT: LIU, CHUAN-PA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHY
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 12
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-12

Query Match      98.0%; Score 248; DB 11; Length 78;
Best Local Similarity 98.0%; Pred. No. 5.8e-25;
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

Qy	1	F	V	A	L	G	A	P	L	A	P	R	D	A	G	S	O	R	P	K	K	E	D	N	V	L	V	E	S	H	E	K	S	L	G	E	A	N	K	A	D	N	V	L	T	K	A	S	Q	51						
Db	28	F	V	A	L	G	A	P	L	A	P	R	D	A	G	S	O	R	P	K <td>K <td>E <td>D <td>N <td>V <td>L <td>V <td>E <td>S <td>H <td>E <td>K <td>S <td>L <td>G <td>E <td>A <td>N <td>K <td>A <td>D <td>N <td>V <td>L <td>T <td>K <td>A <td>S <td>Q <td>78</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	K <td>E <td>D <td>N <td>V <td>L <td>V <td>E <td>S <td>H <td>E <td>K <td>S <td>L <td>G <td>E <td>A <td>N <td>K <td>A <td>D <td>N <td>V <td>L <td>T <td>K <td>A <td>S <td>Q <td>78</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	E <td>D <td>N <td>V <td>L <td>V <td>E <td>S <td>H <td>E <td>K <td>S <td>L <td>G <td>E <td>A <td>N <td>K <td>A <td>D <td>N <td>V <td>L <td>T <td>K <td>A <td>S <td>Q <td>78</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	D <td>N <td>V <td>L <td>V <td>E <td>S <td>H <td>E <td>K <td>S <td>L <td>G <td>E <td>A <td>N <td>K <td>A <td>D <td>N <td>V <td>L <td>T <td>K <td>A <td>S <td>Q <td>78</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	N <td>V <td>L <td>V <td>E <td>S <td>H <td>E <td>K <td>S <td>L <td>G <td>E <td>A <td>N <td>K <td>A <td>D <td>N <td>V <td>L <td>T <td>K <td>A <td>S <td>Q <td>78</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	V <td>L <td>V <td>E <td>S <td>H <td>E <td>K <td>S <td>L <td>G <td>E <td>A <td>N <td>K <td>A <td>D <td>N <td>V <td>L <td>T <td>K <td>A <td>S <td>Q <td>78</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	L <td>V <td>E <td>S <td>H <td>E <td>K <td>S <td>L <td>G <td>E <td>A <td>N <td>K <td>A <td>D <td>N <td>V <td>L <td>T <td>K <td>A <td>S <td>Q <td>78</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	V <td>E <td>S <td>H <td>E <td>K <td>S <td>L <td>G <td>E <td>A <td>N <td>K <td>A <td>D <td>N <td>V <td>L <td>T <td>K <td>A <td>S <td>Q <td>78</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	E <td>S <td>H <td>E <td>K <td>S <td>L <td>G <td>E <td>A <td>N <td>K <td>A <td>D <td>N <td>V <td>L <td>T <td>K <td>A <td>S <td>Q <td>78</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	S <td>H <td>E <td>K <td>S <td>L <td>G <td>E <td>A <td>N <td>K <td>A <td>D <td>N <td>V <td>L <td>T <td>K <td>A <td>S <td>Q <td>78</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	H <td>E <td>K <td>S <td>L <td>G <td>E <td>A <td>N <td>K <td>A <td>D <td>N <td>V <td>L <td>T <td>K <td>A <td>S <td>Q <td>78</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	E <td>K <td>S <td>L <td>G <td>E <td>A <td>N <td>K <td>A <td>D <td>N <td>V <td>L <td>T <td>K <td>A <td>S <td>Q <td>78</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	K <td>S <td>L <td>G <td>E <td>A <td>N <td>K <td>A <td>D <td>N <td>V <td>L <td>T <td>K <td>A <td>S <td>Q <td>78</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	S <td>L <td>G <td>E <td>A <td>N <td>K <td>A <td>D <td>N <td>V <td>L <td>T <td>K <td>A <td>S <td>Q <td>78</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	L <td>G <td>E <td>A <td>N <td>K <td>A <td>D <td>N <td>V <td>L <td>T <td>K <td>A <td>S <td>Q <td>78</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	G <td>E <td>A <td>N <td>K <td>A <td>D <td>N <td>V <td>L <td>T <td>K <td>A <td>S <td>Q <td>78</td> </td></td></td></td></td></td></td></td></td></td></td></td></td></td>	E <td>A <td>N <td>K <td>A <td>D <td>N <td>V <td>L <td>T <td>K <td>A <td>S <td>Q <td>78</td> </td></td></td></td></td></td></td></td></td></td></td></td></td>	A <td>N <td>K <td>A <td>D <td>N <td>V <td>L <td>T <td>K <td>A <td>S <td>Q <td>78</td> </td></td></td></td></td></td></td></td></td></td></td></td>	N <td>K <td>A <td>D <td>N <td>V <td>L <td>T <td>K <td>A <td>S <td>Q <td>78</td> </td></td></td></td></td></td></td></td></td></td></td>	K <td>A <td>D <td>N <td>V <td>L <td>T <td>K <td>A <td>S <td>Q <td>78</td> </td></td></td></td></td></td></td></td></td></td>	A <td>D <td>N <td>V <td>L <td>T <td>K <td>A <td>S <td>Q <td>78</td> </td></td></td></td></td></td></td></td></td>	D <td>N <td>V <td>L <td>T <td>K <td>A <td>S <td>Q <td>78</td> </td></td></td></td></td></td></td></td>	N <td>V <td>L <td>T <td>K <td>A <td>S <td>Q <td>78</td> </td></td></td></td></td></td></td>	V <td>L <td>T <td>K <td>A <td>S <td>Q <td>78</td> </td></td></td></td></td></td>	L <td>T <td>K <td>A <td>S <td>Q <td>78</td> </td></td></td></td></td>	T <td>K <td>A <td>S <td>Q <td>78</td> </td></td></td></td>	K <td>A <td>S <td>Q <td>78</td> </td></td></td>	A <td>S <td>Q <td>78</td> </td></td>	S <td>Q <td>78</td> </td>	Q <td>78</td>	78						

RESULT 12

```

US-09-169-786-1
; Sequence 1, Application US/09169786B
; Patent No. US2002025929A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Masahiko
; TITLE OF INVENTION: METHOD OF BUILDING AND MAINTAINING BONE
; FILE REFERENCE: X-11480
; CURRENT APPLICATION NUMBER: US/09/169,786B
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,800
; EARLIER FILING DATE: 1997-10-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-169-786-1

```

Query Match 98.0%; Score 248; DB 9; Length 84;
Best Local Similarity 98.0%; Pred. No. 6.4e-25;
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1 FVALGAPLAPRDAGSORPKKEDNVLVESHEKSLGEANKADVNLTKAKSQ 51 :
Db	34 FVALGAPLAPRDAGSORPKKEDNVLVESHEKSLGEADKADVNLTKAKSQ 84

RESULT 13

RE-002-13
 US-09-843-221A-10
 ; Sequence 10, Application US/09843221A
 ; Publication NO. US20030039654A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KOSTENIUK, PAUL
 ; APPLICANT: LIU, CHUAN-FA
 ; APPLICANT: LACEY, DAVID LEE
 ; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND PARATHYROID
 ; TITLE OF INVENTION: RELATED PROTEIN
 ; FILE REFERENCE: A-665B
 ; CURRENT APPLICATION NUMBER: US/09/843,221A
 ; CURRENT FILING DATE: 2001-04-26
 ; PRIOR APPLICATION NUMBER: 60/266,673
 ; PRIOR FILING DATE: 2001-02-06
 ; PRIOR APPLICATION NUMBER: 60/214,860
 ; PRIOR FILING DATE: 2000-06-28
 ; PRIOR APPLICATION NUMBER: 60/200,053
 ; PRIOR FILING DATE: 2000-04-27
 ; NUMBER OF SEQ ID NOS: 170
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 10
 ; LENGTH: 84
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-843-221A-10

Query Match 98.0%; Score 248; DB 11; Length 84;
Best Local Similarity 98.0%; Pred. No. 6.4e-25;
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

	OY	1 FVALGAPLPRDAGSQRPKKEDNVLVESHEKSLGEANKADVNLTAKSQ	51
		:	
	D8	34 FVALGAPLPRDAGSQRPKKEDNVLVESHEKSLGEADKADVNLTAKSQ	84

RESULT 14

US-09-898-398-1
; Sequence 1, Application US/09898398

```

; Publication No. US20030082179A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Hutchinson, James Scott
;
; TITLE OF INVENTION: PARATHYROID HORMONE ANTIBODIES AND RELATED METHODS
;
; FILE REFERENCE: A1713
;
; CURRENT APPLICATION NUMBER: US/09/898,398
;
; CURRENT FILING DATE: 2001-07-03
;
; NUMBER OF SEQ ID NOS: 8
;
; SOFTWARE: PatentIn version 3.1
;
; SEQ ID NO 1
;
; LENGTH: 84
;
; TYPE: PRT
;
; ORGANISM: Homo sapiens
;
; US-09-898-398-1

```

Query Match	98.0%	Score 248;	DB 11;	Length 84;
Best Local Similarity	98.0%	Pred. NO. 6.4e-25;		
Matches 50;	Conservative	1;	Mismatches 0;	Indels 0; Gaps 0;

QY	1	F	V	A	L	G	A	P	L	A	P	R	D	A	G	S	R	P	K	K	E	D	N	V	L	S	E	H	K	S	L	G	E	A	N	K	A	D	N	V	L	T	K	A	S	Q	51
		:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:			
Db	34	F	V	A	L	G	A	P	L	A	P	R	D	A	G	S	R	P	K	K	E	D	N	V	L	S	E	H	K	S	L	G	E	A	D	K	A	D	N	V	L	T	K	A	S	Q	84

RESULT 15

```

US-10-157-031-50
; Sequence 50, Application US/10157031
; Publication No. US20030108890A1
; GENERAL INFORMATION:
; APPLICANT: Baranova, A. V.
; APPLICANT: Yanukovsky, N. K.
; APPLICANT: Kozlov, A. P.
; APPLICANT: Lobashev, A. V.
; APPLICANT: Krukovskaya, L. L.
; TITLE OF INVENTION: In silico screen
; FILE REFERENCE: 2760-103
; CURRENT APPLICATION NUMBER: US/10/157031
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 415
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
; LENGTH: 115
; TYPE: prt
; ORGANISM: Homo sapiens
US-10-157-031-50

```

```
Query Match      98.0%; Score 248; DB 15; Length 115;
Best Local Similarity 98.0%; Pred. No. 9.3e-25;
Matches 50; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

	QY	1 FVALGAPLAPRDAGSQRP RKEDNVLVESHEKSLGEANKADVNLTKAQSO 51
	Dd	65 FVALGAPLAPRDAGSQRP RKEDNVLVESHEKSLGEAKDADVNLTKAQSO 115

Search completed: October 9, 2003, 08:19:28
Job time : 95.1493 secs